GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 792.231 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGGTTTTTTT.....AAAGTAGCATGGCTGCCCAG 141

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	141	100.0	383	9	AH013410S8	L42634 Homo sapien
2	141	100.0	3083	6	AR144466	AR144466 Sequence
3	141	100.0	3083	6	AR342446	AR342446 Sequence
4	139.4	98.9	2763	6	AR059583	AR059583 Sequence
5	139.4	98.9	2763	6	I28320	I28320 Sequence 1
6	139.4	98.9	2763	6	AR473576	AR473576 Sequence
7	139.4	98.9	2763	6	AR474046	AR474046 Sequence
8	139.4	98.9	168656	9	AL359922	AL359922 Human DNA
9	139.4	98.9	250000	9	AB060808	Homo sapi
c 10	64	45.4	225782	2	AC109529	AC109529 Rattus no
c 11	64	45.4	287775	2	AC108638	AC108638 Rattus no
12	60.2	42.7	499	6	AR425810	AR425810 Sequence
13	60.2	42.7	499	6	AX986504	AX986504 Sequence
14	60.2	42.7	499	6	BD121363	BD121363 EST and e
15	60.2	42.7	1021	9	L40432	L40432 Homo sapien
16	60.2	42.7	1890	9	BC026106	BC026106 Homo sapi
17	60.2	42.7	2269	9	HSU22233	U22233 Human methy
c 18	56	39.7	194025	10	AL831719	AL831719 Mouse DNA
19	54.2	38.4	870	6	AX826996	AX826996 Sequence
20	48.4	34.3	313	6	AX915265	AX915265 Sequence
21	48.4	34.3	313	6	BD050798	BD050798 Sequence
22	45	31.9	1055	10	AB056100	AB056100 Mus muscu
23	45	31.9	2565	10	BC003858	BC003858 Mus muscu
24	44.6	31.6	144832	2	CR545471	CR545471 Danio rer
c 25	44.6	31.6	204824	2	CR388175	CR388175 Danio rer
26	42.2	29.9	852	9	CR541670	CR541670 Homo sapi
27	39.2	27.8	849	9	CR541710	CR541710 Homo sapi
c 28	38.6	27.4	206136	9	AC068037	AC068037 Homo sapi
29	38.2	27.1	175561	9	AC012636	AC012636 Homo sapi
c 30	37.8	26.8	220885	2	AC095404	AC095404 Rattus no
c 31	37.8	26.8	243174	2	AC107550	AC107550 Rattus no
c 32	37.8	26.8	255300	2	AC128061	AC128061 Rattus no
33	36.8	26.1	246235	2	AC129432	AC129432 Rattus no
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36	36.4	25.8	246205	2	AC097898	AC097898 Rattus no
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c 39	36.2	25.7	240864	2	AC006510	AC006510 Homo sapi
c 40	36	25.5	176899	2	AC084108	AC084108 Mus muscu
c 41	36	25.5	199650	10	AC113481	AC113481 Mus muscu
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c 44	35.6	25.2	129241	9	AL353660	AL353660 Human DNA
c 45	35.6	25.2	164846	2	AC107727	AC107727 Mus muscu

ALIGNMENTS

RESULT 1
AH013410S8
LOCUS AH013410S8 383 bp DNA linear PRI 01-DEC-2003
DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 8 and partial cds.
ACCESSION L42634
VERSION L42634.1 GI:38570314
KEYWORDS .
SEGMENT 8 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 383)
AUTHORS Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.
TITLE Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
MEDLINE 96234115
PUBMED 8650244
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22-p21"
/clone="1"
/tissue_type="placenta"
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/gene="MTAP"
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  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         54 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 113

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db        174 TAAAGTAGCATGGCTGCCCAG 194


RESULT 2
AR144466
LOCUS       AR144466               3083 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6210917.
ACCESSION   AR144466
VERSION     AR144466.1  GI:15106333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A. and Carrera,C.J.
  TITLE     Method for suppressing multiple drug resistance in cancer cells
  JOURNAL   Patent: US 6210917-A 1 03-APR-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2874 TAAAGTAGCATGGCTGCCCAG 2894


RESULT 3
AR342446
LOCUS       AR342446               3083 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 25 from patent US 6576420.
ACCESSION   AR342446
VERSION     AR342446.1  GI:33737456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A., Schmid,M. and Carrera,C.J.
  TITLE     Method for early diagnosis of, and determination of prognosis in,
            cancer
  JOURNAL   Patent: US 6576420-A 25 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .3083
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                     /mol_type="genomic DNA"
ORIGIN

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  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2874 TAAAGTAGCATGGCTGCCCAG 2894


RESULT 4
AR059583
LOCUS       AR059583               2763 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5840505.
ACCESSION   AR059583
VERSION     AR059583.1  GI:5986033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
  TITLE     Method for inhibiting adenylosuccinate synthetase activity in
            methylthioadenosine phosphorylase deficient cells
  JOURNAL   Patent: US 5840505-A 1 24-NOV-1998;
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     source          1. .2763
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ORIGIN

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Db       2188 AATCAAAATCTGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2308 TAAAGTAGCATGGCTGCCCAG 2328
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RESULT 5
I28320
LOCUS       I28320                  2763 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571510.
ACCESSION   I28320
VERSION     I28320.1  GI:1819096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Nobori,T. and Carson,D.A.
  TITLE     Method for selective methionine starvation of malignant cells in
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  JOURNAL   Patent: US 5571510-A 1 05-NOV-1996;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 6
AR473576
LOCUS       AR473576                2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689561.
ACCESSION   AR473576
VERSION     AR473576.1  GI:42711901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Tumor suppressor gene and methods for detection of cancer,
            monitoring of tumor progression and cancer treatment
  JOURNAL   Patent: US 6689561-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 7
AR474046
LOCUS       AR474046                2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689864.
ACCESSION   AR474046
VERSION     AR474046.1  GI:42712799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Cyclin dependent kinase 4 inhibitor
  JOURNAL   Patent: US 6689864-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 8
AL359922
LOCUS       AL359922              168656 bp    DNA     linear   PRI 17-JAN-2001
DEFINITION  Human DNA sequence from clone RP11-70L8 on chromosome 9, complete
            sequence.
ACCESSION   AL359922
VERSION     AL359922.10  GI:12191425
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 168656)
  AUTHORS   Laird,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Jan 13, 2001 this sequence version replaced gi:11878000.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence has been finished according to sequence map criteria
            as follows.  An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated repeat sequence elements.  Where the sequence is
            ambiguous, there is an annotation using the 'unsure' feature key.
            The following abbreviations are used to associate primary accession
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            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr9
            RP11-70L8 is from the library RPCI-11.1 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            This sequence is the entire insert of clone RP11-70L8 The true left
            end of clone RP11-149I2 is at 118787 in this sequence. The true
            right end of clone RP11-473O3 is at 73731 in this sequence.
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /chromosome="9"
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                      /clone_lib="RPCI-11.1"
     misc_feature     98399. .98416
                      /note="Single clone region. Assembly confirmed by
                      restriction digest data."
     misc_feature     98649. .98718
                      /note="Single clone region. Assembly confirmed by
                      restriction digest data."
     misc_feature     157251. .157348
                      /note="Single clone region. L1 repeat. Assembly confirmed
                      by restriction digest data"
ORIGIN

  Query Match             98.9%;  Score 139.4;  DB 9;  Length 168656;
  Best Local Similarity   99.3%;  Pred. No. 8.5e-27;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
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Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
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Db     119349 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 119408

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db     119409 TAAAGTAGCATGGCTGCCCAG 119429


RESULT 9
AB060808
LOCUS       AB060808               250000 bp    DNA     linear   PRI 26-APR-2002
DEFINITION  Homo sapiens gene for p16/CDKN2A, complete cds.
ACCESSION   AB060808
VERSION     AB060808.1  GI:20330501
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kohno,T., Inoue,K., Kitagawa,Y., Hayashi,Y., Matsuo,Y.,
            Mizoguchi,H. and Yokota,J.
  TITLE     Prevalent Involvement of Illegitimate V(D)J Recombination in
            Chromosome 9p21 Deletions in Lymphoid Leukemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 250000)
  AUTHORS   Yokota,J., Kohno,T., Inoue,K. and Kitagawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2001) Takashi Kohno, National Cancer Center
            Research Institute, Biology Division; 1-1, Tsukiji 5-chome,
            Chuo-ku, Tokyo 104-0045, Japan (E-mail:tkkohno@gan2.res.ncc.go.jp,
            Tel:81-3-3542-2511(ex.4652), Fax:81-3-3542-0807)
FEATURES              Location/Qualifiers
     source           1. .250000
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /chromosome="9"
                      /map="9p21"
     gene             complement(join(185617. .185630,188290. .188596,
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                      192072. .192221))
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                      /protein_id="BAB91133.1"
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                      /translation="MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSY
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ORIGIN

  Query Match             98.9%;  Score 139.4;  DB 9;  Length 250000;
  Best Local Similarity   99.3%;  Pred. No. 8e-27;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
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Db      79289 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 79348

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79349 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 79408

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db      79409 TAAAGTAGCATGGCTGCCCAG 79429


RESULT 10
AC109529/c
LOCUS       AC109529               225782 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-276K5, *** SEQUENCING IN PROGRESS
            ***, 3 unordered pieces.
ACCESSION   AC109529
VERSION     AC109529.5  GI:25006711
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 225782)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
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            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 225782)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 225782)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 15, 2002 this sequence version replaced gi:23101222.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GPRK
Center clone name: CH230-276K5
---------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 180465 bases at least Q40
Consensus quality: 184814 bases at least Q30
Consensus quality: 187892 bases at least Q20
Estimated insert size: 188688; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 213023: contig of 213023 bp in length
* 213024 213123: gap of unknown length
* 213124 224002: contig of 10879 bp in length
* 224003 224102: gap of unknown length
* 224103 225782: contig of 1680 bp in length.

FEATURES Location/Qualifiers
source 1. .225782
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-276K5"
misc_feature 1. .1450
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misc_feature 111156. .112668
/note="wgs_contig"
misc_feature 145017. .147149
/note="wgs_contig"
misc_feature 221119. .222830
/note="wgs_contig"
misc_feature 222881. .224002
/note="wgs_contig"

ORIGIN

Query Match 45.4%; Score 64; DB 2; Length 225782;
Best Local Similarity 87.5%; Pred. No. 4.8e-07;
Matches 70; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy         59 ATCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              ||| |||| | ||||||||||||||||| |||||||||| ||||||||||  ||||||||
Db     143673 ATCCCTGCTTACTTTCTTCCTTTCAGAACATGGCCCAGTCTTCTGTTTTACCACCAAGAC 143614

Qy         119 ATTAAAGTAGCATGGCTGCC 138
               ||||||  |||||||||| |
Db     143613 ATTAAAACAGCATGGCTGAC 143594
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RESULT 11
AC108638/c
LOCUS AC108638 287775 bp DNA linear HTG 08-OCT-2002
DEFINITION Rattus norvegicus clone CH230-46K10, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
ACCESSION AC108638
VERSION AC108638.4 GI:23270221
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 287775)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,

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            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
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            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
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            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 287775)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 287775)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 23, 2002 this sequence version replaced gi:21737759.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GPRQ
                Center clone name: CH230-46K10
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 238829 bases at least Q40
                Consensus quality: 241996 bases at least Q30
                Consensus quality: 244256 bases at least Q20
                Estimated insert size: 269456; sum-of-contigs estimation
                Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
            * NOTE: This sequence may represent more than one clone.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    63930: contig of 63930 bp in length
            *    63931    64030: gap of unknown length
            *    64031   117547: contig of 53517 bp in length
            *   117548   117647: gap of unknown length
            *   117648   248038: contig of 130391 bp in length
            *   248039   248138: gap of unknown length
            *   248139   249750: contig of 1612 bp in length
            *   249751   249850: gap of unknown length
            *   249851   278054: contig of 28204 bp in length
            *   278055   278154: gap of unknown length
            *   278155   283612: contig of 5458 bp in length
            *   283613   283712: gap of unknown length
            *   283713   287775: contig of 4063 bp in length.
FEATURES             Location/Qualifiers
     source          1. .287775
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-46K10"
     misc_feature    1. .1029
                     /note="wgs_contig"
ORIGIN

  Query Match             45.4%;  Score 64;  DB 2;  Length 287775;
  Best Local Similarity   87.5%;  Pred. No. 4.6e-07;
  Matches   70;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         59 ATCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              ||| |||| | ||||||||||||||||| |||||||||| |||||||||  ||||||||
Db      16687 ATCCCTGCTTACTTTCTTCCTTTCAGAACATGGCCCAGTCTTCTGTTTTACCACCAAGAC 16628

Qy        119 ATTAAAGTAGCATGGCTGCC 138
              ||||||  |||||||||| |
Db      16627 ATTAAAACAGCATGGCTGAC 16608


RESULT 12
AR425810
LOCUS       AR425810                 499 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17307 from patent US 6639063.
ACCESSION   AR425810
VERSION     AR425810.1  GI:40180920
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 17307 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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  Query Match             42.7%;  Score 60.2;  DB 6;  Length 499;
  Best Local Similarity   89.0%;  Pred. No. 1.3e-05;
  Matches    65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
               |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 402

Qy         129 CATGGCTGCCCAG 141
               |||||||||||||
Db         403 CATGGCTGCCCAG 415


RESULT 13
AX986504
LOCUS       AX986504                 499 bp    DNA     linear   PAT 15-JAN-2004
DEFINITION  Sequence 17307 from Patent EP1104808.
ACCESSION   AX986504
VERSION     AX986504.1  GI:40992644
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
  TITLE     ESTs and encoded human proteins
  JOURNAL   Patent: EP 1104808-A 17307 06-JUN-2001;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 6;  Length 499;
  Best Local Similarity   89.0%;  Pred. No. 1.3e-05;
  Matches    65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
               |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 402

Qy         129 CATGGCTGCCCAG 141
               |||||||||||||
Db         403 CATGGCTGCCCAG 415


RESULT 14
BD121363
LOCUS       BD121363                 499 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  EST and encoded human protein.
ACCESSION   BD121363
VERSION     BD121363.1  GI:23216273
KEYWORDS    JP 2002010789-A/13440.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
  TITLE     EST and encoded human protein
  JOURNAL   Patent: JP 2002010789-A 13440 15-JAN-2002;
            GENSET CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002010789-A/13440
            PD   15-JAN-2002
            PF   07-AUG-2000 JP 2000280989
            PR   05-AUG-1999 US    60/147499
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE  PI
             GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
            C12N15/00
            CC   EST and encoded human protein
            FH   Key             Location/Qualifiers
            FT   source          1. .499
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 6;  Length 499;
  Best Local Similarity   89.0%;  Pred. No. 1.3e-05;
  Matches    65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
               |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         343 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 402

Qy         129 CATGGCTGCCCAG 141
               |||||||||||||
Db         403 CATGGCTGCCCAG 415


RESULT 15
L40432
LOCUS       L40432                   1021 bp    mRNA    linear   PRI 12-DEC-2000
DEFINITION  Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
            complete cds.
ACCESSION   L40432
VERSION     L40432.1  GI:11602391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Genomic cloning of methylthioadenosine phosphorylase: a purine
            metabolic enzyme deficient in multiple different cancers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
  MEDLINE   96234115
   PUBMED   8650244
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
            Research on Aging, and Department of Medicine, University of
            California at San Diego, La Jolla, CA 92093-0663, USA
COMMENT     GSDB:S:39613.
            [Flatfile retrieved from GSDB Thu Dec  7 15:18:48 2000].
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p22-p21"
                     /tissue_type="placenta"
                     /tissue_lib="lambda gt11"
     gene            1. .1021
                     /gene="MTAP"
     CDS             111. .962
                     /gene="MTAP"
                     /EC_number="2.4.2.28"
                     /note="putative"
                     /codon_start=1
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                     /product="methylthioadenosine phosphorylase"
                     /protein_id="AAG38871.1"
                     /db_xref="GI:11602392"
                     /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 9;  Length 1021;
  Best Local Similarity   89.0%;  Pred. No. 1.1e-05;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
               |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||
Db         908 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 967

Qy         129 CATGGCTGCCCAG 141
               |||||||||||||
Db         968 CATGGCTGCCCAG 980


Search completed: February  1, 2005, 13:25:56
Job time : 796.231 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 185.045 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGGTTTTTTT.....AAAGTAGCATGGCTGCCCAG 141

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	141	100.0	3083	2	AAX58284	Aax58284 Human met
	2	141	100.0	3083	8	ABX10818	Abx10818 DNA encod
	3	139.4	98.9	2763	2	AAT15167	Aat15167 Methylthi
	4	139.4	98.9	2763	2	AAQ92813	Aaq92813 Human MTA
	5	139.4	98.9	2763	2	AAT85305	Aat85305 Human met
	6	139.4	98.9	2763	2	AAZ00866	Aaz00866 Human MTA
	7	139.4	98.9	2763	5	AAF86091	Aaf86091 Methylthi
	8	139.4	98.9	2763	10	AAD64097	Aad64097 Human met
	9	139.4	98.9	2784	2	AAQ99202	Aaq99202 Pseudomon
c	10	61.8	43.8	603	6	ABQ59540	Abq59540 Human col
	11	61.4	43.5	1437	4	AAH33683	Aah33683 Human col
	12	60.2	42.7	2197	10	ADC30327	Adc30327 Human nov
	13	54.2	38.4	870	10	ADC37133	Adc37133 Cloned me
	14	48.4	34.3	313	3	AAC27053	Aac27053 Human sec
	15	38.2	27.1	175561	8	AAD55694	Aad55694 Human THB
	16	38.2	27.1	175561	12	ADL08129	Adl08129 Human gen
c	17	34.8	24.7	846	8	ACA23147	Aca23147 Prokaryot
c	18	34.8	24.7	66743	4	ABL27118	Abl27118 Drosophil
c	19	34.8	24.7	110000	2	AAX20248_02	Continuation (3 of
c	20	34.8	24.7	110000	2	AAX20248_03	Continuation (4 of
c	21	34	24.1	615	9	ADA48882	Ada48882 Banana ge
c	22	33.6	23.8	581	10	ADB51702	Adb51702 Primary r
	23	32.8	23.3	110000	6	ABA03041_19	Continuation (20 o
c	24	32.4	23.0	2243	5	AAS64245	Aas64245 DNA encod
c	25	32.4	23.0	110000	2	AAX91990_03	Continuation (4 of
	26	32.4	23.0	273254	3	AAC81914	Aac81914 Chlamydia
c	27	32.2	22.8	1076	4	ABL16913	Abl16913 Drosophil
c	28	32.2	22.8	3445	4	ABL16912	Abl16912 Drosophil
c	29	32	22.7	32	3	AAZ35375	Aaz35375 Methylthi
c	30	31.6	22.4	56153	4	AAS46793	Aas46793 Tumour su
	31	31.2	22.1	1943	6	ABZ15340	Abz15340 Arabidops
	32	31.2	22.1	1943	8	ADA68888	Ada68888 Arabidops
	33	31.2	22.1	164702	8	ACF62730	Acf62730 Cancer ba
	34	31.2	22.1	164702	8	ADB20845	Adb20845 MRP1 base
	35	31.2	22.1	164702	10	ADB87934	Adb87934 Human UGT
	36	31.2	22.1	164702	10	ADB96917	Adb96917 Human MDR
	37	31.2	22.1	164702	10	ADB92108	Adb92108 Human MDR
c	38	31	22.0	592	4	AAK67916	Aak67916 Human imm
c	39	31	22.0	655	4	AAK64493	Aak64493 Human imm
c	40	31	22.0	1461	4	AAK67917	Aak67917 Human imm
	41	31	22.0	4632	10	ADB79786	Adb79786 Rat amino
	42	31	22.0	4632	12	ADP72772	Adp72772 Renal tox
c	43	31	22.0	5173	6	ABL32951	Abl32951 Human imm
c	44	30.8	21.8	430	9	ACC72415	Acc72415 Human cDN
c	45	30.8	21.8	501	4	AAS24644	Aas24644 Human ova

ALIGNMENTS

RESULT 1
AAX58284
ID AAX58284 standard; DNA; 3083 BP.
XX
AC AAX58284;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human methylthioadenosine phosphorylase genomic DNA.
XX
KW Methylthioadenosine phosphorylase; MTAse; human;
KW multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW therapy; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	119. .2876
FT		/*tag= a
FT		/note= "contains introns"
FT	exon	119. .151
FT		/*tag= b
FT		/number= 1
FT	intron	152. .449
FT		/*tag= c
FT		/number= 1
FT	exon	450. .536
FT		/*tag= d
FT		/number= 2
FT	intron	537. .723
FT		/*tag= e
FT		/number= 2
FT	exon	724. .782
FT		/*tag= f
FT		/number= 3
FT	intron	783. .898
FT		/*tag= g
FT		/number= 3
FT	exon	899. .1067
FT		/*tag= h
FT		/number= 4
FT	intron	1068. .1377
FT		/*tag= i
FT		/number= 4

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FT   exon            1378. .1480
FT                   /*tag=  j
FT                   /number= 5
FT   intron          1481. .1763
FT                   /*tag=  k
FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag=  l
FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag=  m
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag=  n
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag=  o
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag=  p
FT                   /number= 8
XX
PN   WO9920791-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022557.
XX
PR   23-OCT-1997;   97US-00956657.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Cottam HB,  Nobori T,  Carrera CJ;
XX
DR   WPI; 1999-302753/25.
XX
PT   Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT   leukemia's.
XX
PS   Example 3; Page 42-44; 45pp; English.
XX
CC   This is the DNA sequence of a human methylthioadenosine phosphorylase
CC   (MTAse) genomic DNA clone that was isolated from a cosmid gene library
CC   using an MTAse cDNA probe. The encoded enzyme catabolises
CC   methylthioadenosine to adenine for endogenous salvage incorporation into
CC   the intracellular AMP pool. The invention relates to methods for treating
CC   and preventing the onset and maintenance of multiple drug resistance
CC   (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC   cells are depleted of AMP and ATP and are thus unable to supprt P-
CC   glycoprotein activity. One method obtains a population of target cells
CC   from a host and assays for loss of MTAse activity. MTAse deficient cells
CC   are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC   starves the cells of adenine and suppresses P-glycoprotein activity. The
CC   MTAse deficient host cells are preferably primary tumour cells comprising
CC   small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC   cells or urothelial tumor cells, preferably in humans. MTAse competent
CC   cells are also treated for MDR with purine synthesis inhibitors. MTAse
CC   competent and deficient cells are also treated for malignancy with other
CC   anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC   to detect the presence or absence of MTAse in malignant cell lines
XX
SQ   Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;

  Query Match             100.0%;  Score 141;  DB 2;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-31;
  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2813

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2873

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
               |||||||||||||||||||||
Db       2874 TAAAGTAGCATGGCTGCCCAG 2894


RESULT 2
ABX10818
ID   ABX10818 standard; DNA; 3083 BP.
XX
AC   ABX10818;
XX
DT   17-APR-2003  (first entry)
XX
DE   DNA encoding rat methylthioadenosine phosphorylase (MTAse).
XX
KW   Rat; methylthioadenosine phosphorylase; MTAse; detection;
KW   Rangione method; gene; ds.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   exon            119. .151
FT                   /*tag=  a
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag=  b
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag=  a
FT                   /number= 2
FT   intron          537. .723
FT                   /*tag=  b
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag=  a
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag=  b
FT                   /number= 3
FT   exon            899. .1066
FT                   /*tag=  a
FT                   /number= 4
FT   intron          1067. .1377
FT                   /*tag=  b
FT                   /number= 4
FT   exon            1378. .1480
FT                   /*tag=  a
FT                   /number= 5
FT   intron          1481. .1763
FT                   /*tag=  b
FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag=  a
FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag=  b
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag=  a
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag=  b
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag=  a
FT                   /number= 8
XX
PN   US2002146695-A1.
XX
PD   10-OCT-2002.
XX
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PF   09-FEB-2001; 2001US-00780114.
XX
PR   29-DEC-1993;   93US-00176855.
PR   02-JUN-1995;   95US-00459343.
PR   04-MAY-1998;   98US-00072914.
XX
PA   (NOBO/) NOBORI T.
PA   (CARS/) CARSON D A.
PA   (TAKA/) TAKABAYASHI K.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 2003-208976/20.
XX
PT   Detection of methylthioadenosine phosphorylase presence in mammalian
PT   cells, by adding to sample oligonucleotide probes capable of hybridizing
PT   to methylthioadenosine phosphorylase encoding nucleic acid.
XX
PS   Claim 7; Fig 1; 16pp; English.
XX
CC   The invention describes a method of detecting methylthioadenosine
CC   phosphorylase (MTAse) comprising adding oligonucleotide probes
CC   hybridisable to MTAse encoding nucleic acid to an assayable sample of
CC   cells, where the presence of the nucleic acid indicates the presence of
CC   the MTAse in a cell. The inventive method is simple and efficient in
CC   detecting the presence of MTAse in the mammalian cell. The availability
CC   of the recombinant MTAse enables the production of highly pure material
CC   with greater ease and in greater quantities than was obtained using
CC   Rangione method for the isolation and purification of native MTAse. This
CC   sequence encodes rat methylthioadenosine phosphorylase (MTAse)
XX
SQ   Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

  Query Match             100.0%;  Score 141;  DB 8;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-31;
  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2813

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2873

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2874 TAAAGTAGCATGGCTGCCCAG 2894


RESULT 3
AAT15167
ID   AAT15167 standard; DNA; 2763 BP.
XX
AC   AAT15167;
XX
DT   29-JUN-1996  (first entry)
XX
DE   Methylthioadenosine-phosphorylase gene.
XX
KW   Human; methylthioadenosine-phosphorylase; chromosome walking;
KW   interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW   cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW   melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW   non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW   antibody; imaging; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  b
FT   intron          422. .615
FT                   /*tag=  c
FT   exon            616. .720
FT                   /*tag=  d
FT   intron          721. .963
FT                   /*tag=  e
FT   exon            964. .1203
FT                   /*tag=  f
XX
PN   WO9528169-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;   95WO-US004655.
XX
PR   14-APR-1994;   94US-00227800.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 1995-373630/48.
XX
PT   Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT   useful for diagnosis, assessing predisposition and treatment of cancers.
XX
PS   Example 1; Page 96-101; 129pp; English.
XX
CC   The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC   at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC   tumour suppressor gene (AAT15157-58) is located between this gene and an
CC   interferon-alpha gene cluster, and has been isolated by chromosome
CC   walking. The CDK4I gene, probe and primer derivatives and the gene
CC   product may be used in diagnosis of cancer, particularly melanoma
CC   (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC   carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC   or in antitumour antisense oligonucleotide or ribozyme construction.
CC   Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-30;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 4
AAQ92813
ID   AAQ92813 standard; DNA; 2763 BP.
XX
AC   AAQ92813;
XX
DT   25-MAR-2003  (revised)
DT   05-DEC-1995  (first entry)
XX
DE   Human MTAse.
XX
KW   MTAse; methyladenosine-phosphatase; malignancy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

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FT   exon            254. .421
FT                   /*tag= a
FT   exon            616. .720
FT                   /*tag= b
FT   exon            964. .1203
FT                   /*tag= c
FT   exon            1640. .1762
FT                   /*tag= d
FT   exon            2272. .2310
FT                   /*tag= e
XX
PN   WO9518233-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014920.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CIBA ) CIBA GEIGY CORP.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 1995-246398/32.
XX
PT   Detecting methyl:adenosine phosphatase in mammalian cells - by
PT   hybridisation with specific oligonucleotide for detecting malignancy,
PT   also new nucleic acid, expression vectors, derived polypeptide(s) and
PT   antibodies.
XX
PS   Claim 8; Page 34-35; 47pp; English.
XX
CC   A cosmid gene library constructed from human placenta DNA was screened
CC   using a MTAse cDNA probe to isolate a human MTAse genomic clone (sequence
CC   given in AAQ92813). Absence of MTAse from a cell is indicative of
CC   malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-30;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 5
AAT85305
ID   AAT85305 standard; DNA; 2763 BP.
XX
AC   AAT85305;
XX
DT   28-FEB-1998  (first entry)
XX
DE   Human methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   adenylsuccinate synthetase; lung cancer; glioma;
KW   acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS   Homo sapiens.
XX

FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= a
FT                   /number= 1
FT   intron          422. .615
FT                   /*tag= b
FT                   /number= 1
FT   exon            616. .720
FT                   /*tag= c
FT                   /number= 2
FT   intron          721. .963
FT                   /*tag= d
FT                   /number= 2
FT   exon            964. .1203
FT                   /*tag= e
FT                   /number= 3
XX
PN   WO9732994-A1.
XX
PD   12-SEP-1997.
XX
PF   27-JAN-1997;   97WO-US001193.
XX
PR   08-MAR-1996;   96US-00612542.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 1997-470550/43.
XX
PT   Inhibiting adenyl:succinate synthetase activity in methylthio:adenosine
PT   phosphorylase-deficient cells - by treatment with specific inhibitor,
PT   especially L-alanosine, useful for selective killing of MTAse deficient
PT   cancer cells.
XX
PS   Example 3; Page 25-26; 37pp; English.
XX
CC   This DNA sequence comprises human genomic DNA for methylthioadenosine
CC   phosphorylase (MTase), obtained from a cosmid gene library constructed
CC   from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC   method for inhibiting the activity adenylsuccinate synthetase (ASS) in
CC   mammalian cells deficient in MTAse activity involves: (a) determining
CC   that a population of cells obtained from a mammalian host is MTase
CC   deficient; and (b) administering an ASS inhibitor (preferably L-
CC   alanosine) to the host so that the MTase deficient host cells are
CC   depleted of AMP. The method is especially used to treat human MTAse-
CC   deficient primary tumour cells, specifically non-small cell lung cancer,
CC   acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC   MTAse catabolises methylthioadenosine to adenine for endogenous salvage
CC   incorporation into the intracellular AMP pool. The claimed method
CC   deprives the cells of substrate for de novo synthesis of AMP, resulting
CC   in selective killing of these cells. MTAse sequence-specific
CC   oligonuclotides can be used to detect the presence or absence of MTAse in
CC   malignant cell lines
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-30;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328
```

```
RESULT 6
AAZ00866
ID   AAZ00866 standard; DNA; 2763 BP.
XX
AC   AAZ00866;
XX
DT   20-OCT-1999  (first entry)
XX
DE   Human MTAse DNA.
XX
KW   MTAse; methylthioadenosine phosphorylase; human; detection; active;
KW   catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            253. .421
FT                   /*tag=  a
FT                   /number= 1
FT                   /note= "Putative exon"
FT   intron          422. .615
FT                   /*tag=  b
FT                   /number= 1
FT                   /note= "putative intron"
FT   exon            616. .720
FT                   /*tag=  c
FT                   /number= 2
FT                   /note= "putative exon"
FT   intron          721. .963
FT                   /*tag=  d
FT                   /number= 2
FT                   /note= "putative intron"
FT   exon            964. .1203
FT                   /*tag=  e
FT                   /number= 3
FT                   /note= "putative exon"
XX
PN   US5942393-A.
XX
PD   24-AUG-1999.
XX
PF   18-DEC-1996;   96US-00772113.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Takabayashi K,  Carson DA,  Nobori T;
XX
DR   WPI; 1999-507775/42.
XX
PT   Detecting catalytically active and inactive methylthioadenosine
PT   phosphorylase (MTAse) in mammalian cells useful for identifying malignant
PT   cells which are suitable targets for methionine (MET) starvation therapy.
XX
PS   Claim 6; Fig 1; 14pp; English.
XX
CC   This invention describes a novel method for detecting catalytically
CC   active and inactive methylthioadenosine phosphorylase (MTAse) in
CC   mammalian cells, using oligonucleotide probes which hybridize to MTAse
CC   nucleic acid coding regions. Detection of MTAse encoding nucleic acid
CC   indicates the cell has catalytically active MTAse. The method is useful
CC   for detecting malignant cells with a deficient MTAse gene, useful for
CC   identifying malignant cells which are suitable targets for methionine
CC   (MET) starvation therapy. The new method is simple, efficient and
CC   successful at determining MTAse negative cells, unlike prior art
CC   techniques, which include analysis of catalytic activity in cell
CC   cultures, requiring a commercially unavailable radiochemical substrate,
CC   and immunoassays, using MTAse antibodies which are unable to be produced
CC   in sufficient quantities. Recombinant MTAse protein produced using the
CC   new polynucleotide and vector, allows greater and purer production of
CC   MTAse than prior art techniques (using the Rangione method) for isolating
CC   native MTAse. This sequence represents human MTAse encoding DNA which is
CC   used in the method of the invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-30;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 7
AAF86091
ID   AAF86091 standard; DNA; 2763 BP.
XX
AC   AAF86091;
XX
DT   06-JUL-2001  (first entry)
XX
DE   Methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW   cancer; ds.
XX
OS   Unidentified.
XX
PN   US6214571-B1.
XX
PD   10-APR-2001.
XX
PF   24-NOV-1998;   98US-00199137.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 2001-315458/33.
XX
PT   Inhibiting adenine succinate synthetase (ASS) activity in
PT   methylthioadenosine phosphorylase deficient cells of mammalian host
PT   involves administering ASS inhibitor which depletes adenosine 5'
PT   monophosphate in cells.
XX
PS   Disclosure; Fig 1; 17pp; English.
XX
CC   The present invention relates to inhibiting adenyl succinate synthetase
CC   (ASS) activity in methylthioadenosine phosphorylase (MTAse) deficient
CC   cells of mammalian host. The invention may be used as a treatment for
CC   cancer, especially breest and colon cancer
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             98.9%;  Score 139.4;  DB 5;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-30;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
```

```
Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328
```

RESULT 8
AAD64097
ID AAD64097 standard; DNA; 2763 BP.
XX
AC AAD64097;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human methylthioadenosine phosphorylase (MTAse) genomic DNA.
XX
KW Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTAse;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254. .421
FT /*tag= a
FT intron 422. .615
FT /*tag= b
FT exon 616. .720
FT /*tag= c
FT intron 721. .963
FT /*tag= d
FT exon 964. .1203
FT /*tag= e
XX
PN US2003138928-A1.
XX
PD 24-JUL-2003.
XX
PF 18-JUL-2001; 2001US-00908671.
XX
PR 26-AUG-1997; 97US-00921954.
XX
PA (CARS/) CARSON D A.
PA (NOBO/) NOBORI T.
XX
PI Carson DA, Nobori T;
XX
DR WPI; 2003-851737/79.
XX
PT New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
PT for preparing a composition for diagnosing or treating cancer.
XX
PS Example 1; SEQ ID NO 14; 46pp; English.
XX
CC The present invention relates to novel tumour suppressor genes, termed as
CC cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC proteins. The polynucleotides are useful for preparing a composition for
CC diagnosing or treating cancer. Sequences of the invention are also useful
CC in gene therapy. The present sequence is human methylthioadenosine
CC phosphorylase (MTAse) genomic DNA used in the exemplification of the
CC invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 98.9%; Score 139.4; DB 10; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328
```

RESULT 9
AAQ99202
ID AAQ99202 standard; DNA; 2784 BP.
XX
AC AAQ99202;
XX
DT 07-MAR-1996 (first entry)
XX
DE Pseudomonas putida methylthioadenosine-phosphorylase DNA.
XX
KW Enzyme; MTAase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS Pseudomonas putida.
XX
FH Key Location/Qualifiers
FT CDS 1. .2763
FT /*tag= a
XX
PN WO9517908-A1.
XX
PD 06-JUL-1995.
XX
PF 22-DEC-1994; 94WO-US014919.
XX
PR 29-DEC-1993; 93US-00176413.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Nobori T, Carson DA;
XX
DR WPI; 1995-246192/32.
XX
PT Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT negative tumour cells - used in chemotherapy of mammalian malignant
PT cells.
XX
PS Disclosure; Page 27-28; 46pp; English.
XX
CC Antigenic peptides may be generated from this sequence encoding
CC methyladenosine-phosphorylase, which are then used to generate antibodies
CC specific for MTAse. The produced antibodies may be used in an immunoassay
CC for the detection of MTase
XX
SQ Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

Query Match 98.9%; Score 139.4; DB 2; Length 2784;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328
```

```
RESULT 10
ABQ59540/c
ID   ABQ59540 standard; cDNA; 603 BP.
XX
AC   ABQ59540;
XX
DT   02-AUG-2002  (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:3235.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030732.
XX
PR   02-OCT-2000; 2000US-0237271P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Burgess C,  Astle JH,  Carroll E,  Catino TJ,  Dwivedi P,  Molino GA;
PI   Thiaglingam A,  Lewis ME;
XX
DR   WPI; 2002-426115/45.
XX
PT   New isolated nucleic acid that is differentially expressed in cancer
PT   tissues useful for determining the presence of colon cancer in a cell or
PT   tissue type, and in antisense therapy.
XX
PS   Claim 1; Fig 1; 796pp; English.
XX
CC   ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC   encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC   used in antisense therapy. An antibody immunoreactive with a polypeptide
CC   encoded by (I) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide encoded by a
CC   nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC   from (I) can be used for determining the presence of a nucleic acid which
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists
XX
SQ   Sequence 603 BP; 159 A; 119 C; 110 G; 206 T; 0 U; 9 Other;

  Query Match             43.8%;  Score 61.8;  DB 6;  Length 603;
  Best Local Similarity   96.9%;  Pred. No. 3.2e-08;
  Matches   63;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          77 CCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 136
               ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         440 CCTTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 381

Qy         137 CCCAG 141
               |||||
Db         380 CCCAG 376


RESULT 11
AAH33683
ID   AAH33683 standard; cDNA; 1437 BP.
XX
AC   AAH33683;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:739.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 9; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999;   99US-0157137P.
PR   03-NOV-1999;   99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG74252.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 1; Page 2728-2729; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX
SQ   Sequence 1437 BP; 501 A; 202 C; 262 G; 460 T; 0 U; 12 Other;

  Query Match             43.5%;  Score 61.4;  DB 4;  Length 1437;
  Best Local Similarity   89.0%;  Pred. No. 5.1e-08;
  Matches   65;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
               |||  :|  | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db         104 CCTCCMTAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 163

Qy         129 CATGGCTGCCCAG 141
               |||||||||||||
Db         164 CATGGCTGCCCAG 176


RESULT 12
ADC30327
ID   ADC30327 standard; cDNA; 2197 BP.
XX
AC   ADC30327;
XX
```

DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:409.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 3; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI; 2003-371981/35.
DR P-PSDB; ADC31298.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Claim 1; SEQ ID NO 409; 1185pp; English.
XX
CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of peventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Match 42.7%; Score 60.2; DB 10; Length 2197;
Best Local Similarity 89.0%; Pred. No. 1.2e-07;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
||| | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 858 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 917

Qy 129 CATGGCTGCCCAG 141
||||||||||||
Db 918 CATGGCTGCCCAG 930

RESULT 13
ADC37133
ID ADC37133 standard; cDNA; 870 BP.
XX
AC ADC37133;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cloned methylthioadenosine phosphorylase, MTAP, cDNA.
XX
KW combination therapy; methylthioadenosine phosphorylase; MTAP; inhibitor;
KW glycinamide ribonucleotide formyltransferase; GARFT;
KW aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX
OS Unidentified.
XX
PN WO2003074083-A1.
XX
PD 12-SEP-2003.
XX
PF 17-FEB-2003; 2003WO-IB000615.
XX
PR 04-MAR-2002; 2002US-0361645P.
PR 09-DEC-2002; 2002US-0432275P.
XX
PA (PFIZ) PFIZER INC.
XX
PI Bloom LA, Boritzki TJ, Kung P, Ogden RC, Skalitzky DJ;
PI Zehnder LR, Kuhn LA, Meng JJ;
XX
DR WPI; 2003-748252/70.
XX
PT Selectively killing methylthioadenosine phosphorylase deficient cells
PT used for treating cell proliferative disorders comprises administering
PT glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX
PS Example 3B; Page 182-183; 189pp; English.
XX
CC This invention relates to novel combination therapies that selectively
CC kill methylthioadenosine phosphorylase (MTAP) deficient cells. The
CC combination therapies comprise administering an inhibitor of glycinamide
CC ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC toxicity agent during and after administration of the inhibitor. The
CC combination therapies can be used for selectively killing MTAP deficient
CC cells, and for treating cell proliferative disorders e.g. lung cancer,
CC leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC dose of the inhibitor. This polynucleotide sequence represents the cloned
CC MTAP cDNA of the invention.
XX
SQ Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

Query Match 38.4%; Score 54.2; DB 10; Length 870;

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  Best Local Similarity   88.1%;  Pred. No. 5.6e-06;
  Matches   59;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | | ||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 863

Qy        129 CATGGCT 135
              |||||||
Db        864 CATGGCT 870


RESULT 14
AAC27053
ID   AAC27053 standard; cDNA; 313 BP.
XX
AC   AAC27053;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 31128.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS   Claim 1; SEQ ID NO 31128; 71pp + Sequence Listing; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC   ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC   to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC   diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors
XX
SQ   Sequence 313 BP; 99 A; 50 C; 68 G; 96 T; 0 U; 0 Other;

  Query Match             34.3%;  Score 48.4;  DB 3;  Length 313;
  Best Local Similarity   98.0%;  Pred. No. 0.00022;
  Matches   49;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAAC 50
              |||||||||||| ||||||||||||||||||||||||||||||||||||
Db        262 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAAC 311


RESULT 15
AAD55694
ID   AAD55694 standard; DNA; 175561 BP.
XX
AC   AAD55694;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human THBS4 reference gene (GI 14916146).
XX
KW   Human; thrombospondin 4; THBS4; vascular disease; therapy; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(105290,C)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
FT   variation       replace(118019,A)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO2003020120-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-US028281.
XX
PR   04-SEP-2001; 2001US-0317033P.
PR   17-OCT-2001; 2001US-0330248P.
PR   14-DEC-2001; 2001US-00017721.
XX
PA   (VITI-) VITIVITY INC.
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Mccarthy J,  Daley G,  Bolk S;
XX
DR   WPI; 2003-312992/30.
XX
PT   Novel isolated nucleic acid comprising allelic variant of polymorphic
PT   region of thrombospondin 1 or 4 gene, useful for identifying
PT   predisposition of subject to develop vascular disease associated with the
PT   allelic variant.
XX
PS   Claim 64; Fig 3; 338pp; English.
XX
CC   The invention is based at least in part on the discovery of polymorphisms
CC   within the thrombospondin 1 (THBS1) or THBS4 genes. The invention also
CC   provides a nucleic acid comprising allelic variant of polymorphic region
CC   of THBS1 or THBS4 gene. The method is useful for identifying a subject as
CC   a candidate for a particular clinical course of therapy or to treat a
CC   vascular disease or disorder and for selecting a clinical course of
CC   therapy to treat a subject who is at risk for developing a vascular
CC   disease or disorder. The present sequence is human THBS4 reference gene.
CC   Note: This sequence is said to encode SEQ ID NO: 4 (AAE36229). However
CC   this does not appear to be the case
XX
SQ   Sequence 175561 BP; 51351 A; 37974 C; 36559 G; 49677 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 38.2;  DB 8;  Length 175561;
  Best Local Similarity   58.3%;  Pred. No. 0.8;
  Matches   67;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          9 TCTGGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATATCACTGCCT 68
              | ||||||| ||||||| |||| ||||    | |     |   ||     | |   || |
Db       3596 TATGGTTTTGTTTTTAAACAACACCTCATCTTTGAAATGACTCTGCTGGAAACCTAGCAT 3655

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 123
              ||| ||  |||||||||||  ||    | | | ||  |||  | | ||||| |
Db       3656 TTTTTTTTTTTTTCAGAATATTTCCACTGTGTATATTAAATTGACTAAACATTCA 3710
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Search completed: February 1, 2005, 12:39:36
Job time : 188.045 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 41.1846 Seconds
(without alignments)
2433.465 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGGTTTTTTT.....AAAGTAGCATGGCTGCCCAG 141

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	141	100.0	3083	3	US-08-956-657-1	Sequence 1, Appli
2	141	100.0	3083	4	US-09-335-231-25	Sequence 25, Appl
3	139.4	98.9	2763	1	US-08-176-413-1	Sequence 1, Appli
4	139.4	98.9	2763	2	US-08-612-542B-1	Sequence 1, Appli
5	139.4	98.9	2763	2	US-08-772-113-1	Sequence 1, Appli
6	139.4	98.9	2763	3	US-09-199-137-1	Sequence 1, Appli
7	139.4	98.9	2763	4	US-08-227-800A-14	Sequence 14, Appl
8	139.4	98.9	2763	4	US-08-921-954-14	Sequence 14, Appl
9	139.4	98.9	2763	5	PCT-US94-14919-1	Sequence 1, Appli
10	139.4	98.9	2763	5	PCT-US94-14920-1	Sequence 1, Appli
11	60.2	42.7	499	4	US-09-621-976-17307	Sequence 17307, A
12	48.4	34.3	313	4	US-09-513-999C-31128	Sequence 31128, A
c 13	32.4	23.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 14	32	22.7	32	4	US-09-335-231-24	Sequence 24, Appl
15	30.6	21.7	700	3	US-08-998-416-302	Sequence 302, App
16	30.6	21.7	714	3	US-08-998-416-863	Sequence 863, App
17	30.6	21.7	714	3	US-08-998-416-1139	Sequence 1139, Ap
18	30.6	21.7	722	3	US-08-998-416-680	Sequence 680, App
19	30.6	21.7	725	3	US-08-998-416-1051	Sequence 1051, Ap
20	30.6	21.7	761	3	US-08-998-416-382	Sequence 382, App
21	29.2	20.7	4612	4	US-09-626-301-1	Sequence 1, Appli
22	29.2	20.7	4642	4	US-09-626-301-3	Sequence 3, Appli
c 23	29	20.6	4261	4	US-09-976-594-3	Sequence 3, Appli
c 24	28.8	20.4	3001	3	US-09-387-212-9	Sequence 9, Appli
c 25	28.8	20.4	3001	4	US-09-948-802-9	Sequence 9, Appli
26	28.8	20.4	3552	4	US-09-643-597-126	Sequence 126, App
27	28.8	20.4	3552	4	US-09-480-884A-126	Sequence 126, App
28	28.8	20.4	3552	4	US-09-542-615A-126	Sequence 126, App
29	28.8	20.4	3552	4	US-09-606-421B-126	Sequence 126, App
30	28.8	20.4	3552	4	US-09-221-107-126	Sequence 126, App
31	28.8	20.4	3552	4	US-09-466-396A-126	Sequence 126, App
32	28.8	20.4	3552	4	US-09-476-496A-126	Sequence 126, App
33	28.8	20.4	3552	4	US-09-630-940B-126	Sequence 126, App
34	28.6	20.3	1609	4	US-09-976-594-550	Sequence 550, App
35	28.6	20.3	2172	4	US-09-976-594-125	Sequence 125, App
36	28.6	20.3	5156	2	US-09-091-432-3	Sequence 3, Appli
37	28.6	20.3	5156	4	US-09-387-663-3	Sequence 3, Appli
38	28.6	20.3	5156	4	US-09-214-139B-3	Sequence 3, Appli
39	28.6	20.3	5762	4	US-09-919-172-55	Sequence 55, Appl
40	28.4	20.1	335	4	US-09-270-767-2649	Sequence 2649, Ap
41	28.4	20.1	335	4	US-09-270-767-17931	Sequence 17931, A
c 42	28.4	20.1	1093	4	US-09-257-179-35	Sequence 35, Appl
43	28.4	20.1	640681	4	US-09-790-988-1	Sequence 1, Appli
c 44	28.4	20.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 45	28.4	20.1	1664976	4	US-09-692-570-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-956-657-1
; Sequence 1, Application US/08956657
; Patent No. 6210917
; GENERAL INFORMATION:
; APPLICANT: No. 6210917ori et al., Tsutomu
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,342
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/050001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3083 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-956-657-1

Query Match 100.0%; Score 141; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 6.8e-33;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
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Db       2754 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2813

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2873

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2874 TAAAGTAGCATGGCTGCCCAG 2894
```

RESULT 2
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 02307O-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTAP) gene
; NAME/KEY: modified_base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
US-09-335-231-25

Query Match 100.0%; Score 141; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 6.8e-33;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
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Qy        121 TAAAGTAGCATGGCTGCCCAG 141
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Db       2874 TAAAGTAGCATGGCTGCCCAG 2894
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RESULT 3
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,413
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD2864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
US-08-176-413-1

Query Match 98.9%; Score 139.4; DB 1; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
```

```
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 4
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
;  GENERAL INFORMATION:
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    APPLICANT:  No. 5840505ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    TITLE OF INVENTION:  METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
;    TITLE OF INVENTION:  ACTIVITY IN MALIGNANT METHYLTHIOADENOSINE PHOSPHORYLASE DEFICI
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,542B
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-612-542B-1

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 5
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5942393ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Takabayashi, Kenji
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/772,113
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,855
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-772-113-1

  Query Match             98.9%;  Score 139.4;  DB 2;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 6
US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6214571ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Carrera, Carlos J.
```

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;    APPLICANT:  Cottam, Howard B.
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,137
;      FILING DATE:  24-NOV-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-09-199-137-1

  Query Match             98.9%;  Score 139.4;  DB 3;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 7
US-08-227-800A-14
; Sequence 14, Application US/08227800A
; Patent No. 6689561
;  GENERAL INFORMATION:
;    APPLICANT:  CARSON, DENNIS A.
;    APPLICANT:  NOBORI, TSUTOMU
;    TITLE OF INVENTION:  TUMOR SUPPRESSOR GENE AND METHODS FOR
;    TITLE OF INVENTION:  DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANCE
;    TITLE OF INVENTION:  TREATMENT
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,800A
;      FILING DATE:  14-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOWELLS, STACY L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/023001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Methylthioadenosine Phosphorylase (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-227-800A-14

  Query Match             98.9%;  Score 139.4;  DB 4;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 8
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
;   GENERAL INFORMATION:
;        APPLICANT: Carson, Dennis A.
;                   No. 6689864ori, Tsutomu
;        TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
;                            Detection of Cancer, Monitoring of Tumor Progression and
;                            Cancer Treatment
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
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;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/921,954
;             FILING DATE: 26-Aug-1997
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671A
;             FILING DATE: 18-Jul-2001
;             APPLICATION NUMBER: US 08/921,954
;             FILING DATE: 20-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Hinsch, Matthew E.
;             REGISTRATION NUMBER: 47,651
;             REFERENCE/DOCKET NUMBER: 02307O-104042US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;             NAME/KEY:  -
;             LOCATION:  1..2763
;             OTHER INFORMATION:  /note= "full-length
;             methylthioadenosine phosphorylase
;             (MTAse) genomic nucleotide sequence"
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  254..421
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  616..720
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  964..1203
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

  Query Match             98.9%;  Score 139.4;  DB 4;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 9
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR SELECTIVE METHIONINE
;    TITLE OF INVENTION:  STARVATION OF MALIGNANT CELLS IN MAMMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14919
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-286
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14919-1

  Query Match             98.9%;  Score 139.4;  DB 5;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 10
PCT-US94-14920-1
; Sequence 1, Application PC/TUS9414920
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14920
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-287
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14920-1

  Query Match             98.9%;  Score 139.4;  DB 5;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 2e-32;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
              |||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 11
US-09-621-976-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 17307
;   LENGTH: 499
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-17307

  Query Match             42.7%;  Score 60.2;  DB 4;  Length 499;
  Best Local Similarity   89.0%;  Pred. No. 5e-09;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||
Db        343 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 402

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        403 CATGGCTGCCCAG 415


RESULT 12
US-09-513-999C-31128
; Sequence 31128, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 31128
;   LENGTH: 313
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-31128

  Query Match             34.3%;  Score 48.4;  DB 4;  Length 313;
  Best Local Similarity   98.0%;  Pred. No. 1.4e-05;
  Matches   49;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAAC 50
              ||||||||||| |||||||||||||||||||||||||||||||||||||
Db        262 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAAC 311


RESULT 13
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (15001)..(30000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (30001)..(45000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (60001)..(75000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (75001)..(90000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (90001)..(105000)
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;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (105001)..(120000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (120001)..(135000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (135001)..(150000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (150001)..(165000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (165001)..(180000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (195001)..(210000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (270001)..(285000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
;   LOCATION: (345001)..(360000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
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;   NAME/KEY: misc_feature

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  Best Local Similarity   56.6%;  Pred. No. 8;
  Matches   60;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

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RESULT 14
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; Sequence 24, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE:  02307O-108010US
;  CURRENT APPLICATION NUMBER: US/09/335,231
;  CURRENT FILING DATE:  1999-06-17
;  PRIOR APPLICATION NUMBER:  US 60/090,411
;  PRIOR FILING DATE:  1998-06-23
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:anti-sense
;   OTHER INFORMATION: primer
US-09-335-231-24

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  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 15
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; Sequence 302, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  302:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  700 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1248UP
US-08-998-416-302

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              | | | |||| | ||||| | ||| | |||||   || | | |       |||||   |
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Qy        126 TAGCA 130
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Search completed: February  1, 2005, 15:01:01
Job time : 45.1846 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 193.911 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		141	100.0	3083	9	US-09-780-114-1	Sequence 1, Appli
2		141	100.0	3083	15	US-10-326-681-25	Sequence 25, Appl
3		139.4	98.9	2763	10	US-09-908-671-14	Sequence 14, Appl
c 4		61.8	43.8	603	11	US-09-969-034-3235	Sequence 3235, Ap
5		61.4	43.5	1437	15	US-10-106-698-749	Sequence 749, App
6		60.2	42.7	2269	18	US-10-779-476-2	Sequence 2, Appli
7		54.2	38.4	870	16	US-10-367-366-1	Sequence 1, Appli
8		38.2	27.1	175561	14	US-10-017-721-3	Sequence 3, Appli
9		38.2	27.1	175561	16	US-10-235-192A-48	Sequence 48, Appl
c 10		34.8	24.7	846	16	US-10-282-122A-11017	Sequence 11017, A
c 11		33.4	23.7	678	13	US-10-027-632-29328	Sequence 29328, A
c 12		33.4	23.7	678	13	US-10-027-632-29329	Sequence 29329, A
c 13		33.4	23.7	678	15	US-10-027-632-29328	Sequence 29328, A
c 14		33.4	23.7	678	15	US-10-027-632-29329	Sequence 29329, A
c 15		33.4	23.7	808	13	US-10-027-632-31882	Sequence 31882, A
c 16		33.4	23.7	808	15	US-10-027-632-31882	Sequence 31882, A
c 17		33.4	23.7	107320	13	US-10-087-192-1333	Sequence 1333, Ap
c 18		33	23.4	344805	18	US-10-779-271-1	Sequence 1, Appli
19		32.6	23.1	111836	17	US-10-322-281-51	Sequence 51, Appl
c 20		32.4	23.0	1230025	16	US-10-289-762-1	Sequence 1, Appli
c 21		32	22.7	32	15	US-10-326-681-24	Sequence 24, Appl
22		32	22.7	632	13	US-10-027-632-224812	Sequence 224812,
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c 24		31.6	22.4	56153	16	US-10-221-714A-519	Sequence 519, App
c 25		31.4	22.3	2106	16	US-10-425-114-25876	Sequence 25876, A
26		31.2	22.1	1943	9	US-09-938-842A-3145	Sequence 3145, Ap
27		31.2	22.1	1943	11	US-09-938-842A-3145	Sequence 3145, Ap
c 28		31.2	22.1	161484	17	US-10-317-401-4	Sequence 4, Appli
c 29		31.2	22.1	2731748	17	US-10-297-465A-1	Sequence 1, Appli
30		31	22.0	4632	15	US-10-205-219-26	Sequence 26, Appl
c 31		31	22.0	5173	15	US-10-311-455-924	Sequence 924, App
32		30.8	21.8	430	15	US-10-102-524-968	Sequence 968, App
c 33		30.8	21.8	430	15	US-10-264-283-81	Sequence 81, Appl
c 34		30.8	21.8	491	13	US-10-027-632-278572	Sequence 278572,
c 35		30.8	21.8	491	15	US-10-027-632-278572	Sequence 278572,
c 36		30.8	21.8	501	9	US-09-777-564-825	Sequence 825, App
c 37		30.8	21.8	501	9	US-09-777-564-1495	Sequence 1495, Ap
c 38		30.8	21.8	501	14	US-10-015-219-825	Sequence 825, App
c 39		30.8	21.8	501	14	US-10-015-219-1495	Sequence 1495, Ap
c 40		30.8	21.8	1984	14	US-10-198-846-13791	Sequence 13791, A
c 41		30.8	21.8	3641	13	US-10-078-650-1	Sequence 1, Appli
c 42		30.8	21.8	3641	14	US-10-097-340-66	Sequence 66, Appl
c 43		30.8	21.8	3641	15	US-10-102-524-1713	Sequence 1713, Ap
c 44		30.8	21.8	3641	15	US-10-264-283-82	Sequence 82, Appl
c 45		30.8	21.8	5507	18	US-10-473-126-197	Sequence 197, App

ALIGNMENTS

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RESULT 1
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
;  GENERAL INFORMATION:
;       APPLICANT: No. US20020146695A1ori, Tsutomu
;                  Carson, Dennis A.
;                  Takabayashi, Kenji
;       TITLE OF INVENTION: Method for Detection of the Presence or
;                           Absence of Methylthioadenosine Phosphorylase
;                           (MTAse) in a
;                           Cell Sample by Detection of the Presence or Absence
;       NUMBER OF SEQUENCES: 1
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/780,114
;            FILING DATE: 09-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/072,914
;            FILING DATE: 04-May-1998
;            APPLICATION NUMBER: US 08/176,855
;            FILING DATE: 29-DEC-1993
;            APPLICATION NUMBER: US 08/459,343
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;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 08/827,342
;            FILING DATE: 26-MAR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bastian, Kevin L.
;            REGISTRATION NUMBER: 34,774
;            REFERENCE/DOCKET NUMBER: 02307O-103030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3083 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
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;            LOCATION:  1..3083
;            OTHER INFORMATION:  /note= "rat methylthioadenosine
;            phosphorylase (MTAse)"
;       FEATURE:
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;            LOCATION:  119..151
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US-09-780-114-1

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  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE: 02307O-108010US
;  CURRENT APPLICATION NUMBER: US/10/326,681
;  CURRENT FILING DATE:  2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/090,411
;  PRIOR FILING DATE: 1998-06-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   FEATURE:
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;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
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;   LOCATION: (724)..(782)
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;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
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;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
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;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
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;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
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;   NAME/KEY: exon
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;   OTHER INFORMATION: exon 8
US-10-326-681-25

  Query Match             100.0%;  Score 141;  DB 15;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 3e-31;
  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2813

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2873

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
                 |||||||||||||||||||||
Db       2874 TAAAGTAGCATGGCTGCCCAG 2894


RESULT 3
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
;   GENERAL INFORMATION:
;        APPLICANT: CARSON, DENNIS A.
;                   NOBORI, TSUTOMU
;        TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
;                            DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
;                            TREATMENT
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: California
;             COUNTRY: US
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671
;             FILING DATE: 18-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/227,800
;             FILING DATE: 14-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HOWELLS, STACY L.
;             REGISTRATION NUMBER: 34,842
;             REFERENCE/DOCKET NUMBER: 07340/023001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
;             TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        IMMEDIATE SOURCE:
;             CLONE: Methylthioadenosine Phosphorylase (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..2763
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

  Query Match             98.9%;  Score 139.4;  DB 10;  Length 2763;
  Best Local Similarity   99.3%;  Pred. No. 8.5e-31;
  Matches  140;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 2247

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2248 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACAT 2307

Qy        121 TAAAGTAGCATGGCTGCCCAG 141
                 ||||||||||||||||||||
Db       2308 TAAAGTAGCATGGCTGCCCAG 2328


RESULT 4
US-09-969-034-3235/c
; Sequence 3235, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT:  Astle, Jon H.
;  APPLICANT:  Carroll, Eddie III
;  APPLICANT:  Catino, Theodore J.
;  APPLICANT:  Dwivedi, Poornima
;  APPLICANT:  Molino, Gary A.
;  APPLICANT:  Thiagalingam, Arunthathi
;  APPLICANT:  Lewis, Marcia E.
;  TITLE OF INVENTION: Nucleic Acid Sequences Differentially
;  TITLE OF INVENTION:  Expressed in Cancer Tissue
;  FILE REFERENCE: 1657/1032
;  CURRENT APPLICATION NUMBER: US/09/969,034
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: 60/237,271
;  PRIOR FILING DATE: 2000-02-10
;  NUMBER OF SEQ ID NOS: 4494
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3235
;   LENGTH: 603
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 492, 497, 506, 527, 542, 544, 573, 576, 597
;   OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235

  Query Match             43.8%;  Score 61.8;  DB 11;  Length 603;
  Best Local Similarity   96.9%;  Pred. No. 3.7e-08;
  Matches   63;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         77 CCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 136
              ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CCTTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 381

Qy        137 CCCAG 141
                 |||||
Db        380 CCCAG 376


RESULT 5
US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-106-698-749
```

```
  Query Match             43.5%;  Score 61.4;  DB 15;  Length 1437;
  Best Local Similarity   89.0%;  Pred. No. 6.6e-08;
  Matches   65;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||  :|  | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db        104 CCTCCMTAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 163

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        164 CATGGCTGCCCAG 176


RESULT 6
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
;  APPLICANT: Salmedix, Inc.
;  APPLICANT:  Leoni,Lorenzo M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
;  TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
;  FILE REFERENCE: 076936-0307942
;  CURRENT APPLICATION NUMBER: US/10/779,476
;  CURRENT FILING DATE:  2004-02-13
;  PRIOR APPLICATION NUMBER: 60/447,888
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: 60/460,715
;  PRIOR FILING DATE: 2004-04-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-779-476-2

  Query Match             42.7%;  Score 60.2;  DB 18;  Length 2269;
  Best Local Similarity   89.0%;  Pred. No. 1.8e-07;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 978

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        979 CATGGCTGCCCAG 991


RESULT 7
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
;  APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
;  APPLICANT:  Bloom, Laura  A
;  APPLICANT:  Kuhn, Leslie
;  APPLICANT:  Meng, Jerry Jialun
;  APPLICANT:  Kung, Pei-Pei
;  APPLICANT:  Zehnder, Luke
;  APPLICANT:  Boritzki, Theodore  J.
;  APPLICANT:  Ogden, Richard
;  APPLICANT:  Skalitzky , Donald
;  TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
;  TITLE OF INVENTION:  Phosphorylase Deficient Cells
;  FILE REFERENCE: PC19080A (AG110-01)
;  CURRENT APPLICATION NUMBER: US/10/367,366
;  CURRENT FILING DATE:  2003-02-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

  Query Match             38.4%;  Score 54.2;  DB 16;  Length 870;
  Best Local Similarity   88.1%;  Pred. No. 7.3e-06;
  Matches   59;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 863

Qy        129 CATGGCT 135
              |||||||
Db        864 CATGGCT 870


RESULT 8
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
;  APPLICANT: McCarthy, Jeanette
;  APPLICANT:  Daley, George
;  APPLICANT:  Bolk, Stacey
;  TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
;  FILE REFERENCE: MMI-003
;  CURRENT APPLICATION NUMBER: US/10/017,721
;  CURRENT FILING DATE:  2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/317,033
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: US 60/330,248
;  PRIOR FILING DATE: 2001-10-17
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 175561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-721-3

  Query Match             27.1%;  Score 38.2;  DB 14;  Length 175561;
  Best Local Similarity   58.3%;  Pred. No. 2.7;
  Matches   67;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          9 TCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATATCACTGCCT 68
              | ||||||| |||||||  |||| ||||    | |    |   ||     | |   || |
Db       3596 TATGGTTTTGTTTTTAAACAACACCTCATCTTTGAAATGACTCTGCTGGAAACCTAGCAT 3655

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 123
                ||| ||  ||||||||||||  ||    | | | ||  |||  | | ||||| |
Db       3656 TTTTTTTTTTTTTCAGAATATTTCCACTGTGTATATTAAATTGACTAAACATTCA 3710


RESULT 9
US-10-235-192A-48
; Sequence 48, Application US/10235192A
; Publication No. US20040043389A1
; GENERAL INFORMATION:
;  APPLICANT: McCarthy, Jeanette
;  TITLE OF INVENTION: Methods and Compositions for Identifying
;  TITLE OF INVENTION:  Risk Factors for Abnormal Lipid Levels and the Diseases
;  TITLE OF INVENTION:  and Disorders Associated Therewith
;  FILE REFERENCE: MMI-011
;  CURRENT APPLICATION NUMBER: US/10/235,192A
;  CURRENT FILING DATE:  2002-09-04
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 175561
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
US-10-235-192A-48

  Query Match             27.1%;  Score 38.2;  DB 16;  Length 175561;
  Best Local Similarity   58.3%;  Pred. No. 2.7;
  Matches   67;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          9 TCTGGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATATCACTGCCT 68
              | ||||||| ||||||| |||| |||| | |   |  ||    | |  || |
Db       3596 TATGGTTTTGTTTTTAAACAACACCTCATCTTTGAAATGACTCTGCTGGAAACCTAGCAT 3655

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 123
                ||| ||  ||||||||||||  ||    | | | ||  |||  | | ||||| |
Db       3656 TTTTTTTTTTTTTCAGAATATTTCCACTGTGTATATTAAATTGACTAAACATTCA 3710


RESULT 10
US-10-282-122A-11017/c
; Sequence 11017, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11017
;   LENGTH: 846
;   TYPE: DNA
;   ORGANISM: Borrelia burgdorferi
US-10-282-122A-11017

  Query Match             24.7%;  Score 34.8;  DB 16;  Length 846;
  Best Local Similarity   60.6%;  Pred. No. 3.8;
  Matches   57;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy         17 TTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATATCACTGCCTCCTTTCTT 76
              |||||||  |  || ||||||| ||| ||||||    ||        | ||   ||| ||
Db        229 TTTTTTTTAATAAAATCTCAGTCATTGCGCCAAGGCCTGGGCCAATTTCCCAGATTTTTT 170

Qy         77 CCTTTCAGAATATGGCCCAGTTTTCTGTTTTATT 110
                | |||      |||  |  || ||||| || | ||
Db        169 CATTTTCTTTTATATCTAAGCTTTCTATTATTTT 136


RESULT 11
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29328
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-29328

  Query Match             23.7%;  Score 33.4;  DB 13;  Length 678;
  Best Local Similarity   72.9%;  Pred. No. 9;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         60 TCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              || | ||  |   | |||||| |||  |||||||||||||||||||| |   ||| |
Db        351 TCCCAGCTGCTGGTTTTCCTTCCAGCCTATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 12
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
```

```
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29329
;    LENGTH: 678
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-29329

  Query Match             23.7%;  Score 33.4;  DB 13;  Length 678;
  Best Local Similarity   72.9%;  Pred. No. 9;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         60 TCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              || | ||  |   | |||||| |||  |||||||||||||||||||| |   ||| |
Db        351 TCCCAGCTGCTGGTTTTCCTTCCAGCCTATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 13
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29328
;    LENGTH: 678
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-29328

  Query Match             23.7%;  Score 33.4;  DB 15;  Length 678;
  Best Local Similarity   72.9%;  Pred. No. 9;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         60 TCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              || | ||  |   | |||||| |||  |||||||||||||||||||| |   ||| |
Db        351 TCCCAGCTGCTGGTTTTCCTTCCAGCCTATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 14
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29329
;    LENGTH: 678
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-29329

  Query Match             23.7%;  Score 33.4;  DB 15;  Length 678;
  Best Local Similarity   72.9%;  Pred. No. 9;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         60 TCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              || | ||  |   | |||||| |||  |||||||||||||||||||| |   ||| |
Db        351 TCCCAGCTGCTGGTTTTCCTTCCAGCCTATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 15
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31882
;    LENGTH: 808
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-31882

  Query Match             23.7%;  Score 33.4;  DB 13;  Length 808;
  Best Local Similarity   72.9%;  Pred. No. 9.6;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         60 TCACTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGAC 118
              || | ||  |   | |||||| |||  |||||||||||||||||||| |   ||| |
Db        351 TCCCAGCTGCTGGTTTTCCTTCCAGCCTATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


Search completed: February  1, 2005, 17:20:31
Job time : 197.911 secs
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 1585.32 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGGTTTTTTT.....AAAGTAGCATGGCTGCCCAG 141

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	91.4	64.8	687	2	AW976322	AW976322 EST388431
	2	61.8	43.8	358	2	BE768971	BE768971 PM4-FT002
	3	61.8	43.8	900	5	BX390237	BX390237 BX390237
	4	61.2	43.4	370	5	BX495614	BX495614 DKFZp779E
c	5	60.2	42.7	257	1	AI919501	AI919501 tp22b01.x
c	6	60.2	42.7	491	1	AA635142	AA635142 af10e10.s
c	7	60.2	42.7	570	6	CD364939	CD364939 UI-H-FT2-
	8	60.2	42.7	612	7	CN409515	CN409515 170006001
	9	60.2	42.7	681	4	BM784030	BM784030 K-EST0062
c	10	60.2	42.7	684	6	CD364946	CD364946 UI-H-FT2-
	11	60.2	42.7	819	2	BF981023	BF981023 602310222
	12	60.2	42.7	836	1	AL048242	AL048242 DKFZp586O
	13	60.2	42.7	836	4	BG574734	BG574734 602596770
c	14	60.2	42.7	903	5	BX371508	BX371508 BX371508
c	15	60.2	42.7	911	5	BX350035	BX350035 BX350035
	16	60.2	42.7	975	4	BM472910	BM472910 AGENCOURT
	17	60.2	42.7	1064	5	BX459089	BX459089 BX459089
	18	60.2	42.7	1380	3	BC012316	BC012316 Homo sapi
	19	59.8	42.4	1075	1	AL543068	AL543068 AL543068
c	20	59.4	42.1	401	1	AI674711	AI674711 wd19e10.x
c	21	57.2	40.6	330	5	BX102948	BX102948 BX102948
	22	55	39.0	659	4	BG572739	BG572739 602594259
	23	54.6	38.7	388	1	AJ686857	AJ686857 AJ686857
c	24	53.8	38.2	429	1	AV667881	AV667881 AV667881
	25	53.8	38.2	477	4	BG938257	BG938257 1Abo14E09
	26	53.8	38.2	484	7	CF930825	CF930825 CF--05-R-
	27	53.8	38.2	562	4	BI774611	BI774611 466793 MA
c	28	53.8	38.2	568	7	CO586973	CO586973 DG2-13911
c	29	53.8	38.2	581	6	CB538214	CB538214 776179 MA
	30	53.8	38.2	586	7	CN441464	CN441464 BE04026A1
c	31	53.8	38.2	600	7	CO701132	CO701132 DG32-195b
	32	53.8	38.2	682	7	CN788377	CN788377 4122709 B
	33	53.8	38.2	950	7	CF413058	CF413058 CH3#083_G
	34	52.8	37.4	609	6	CD535426	CD535426 LeukoN5_4
	35	51.2	36.3	638	7	CN409513	CN409513 170005327
	36	50.6	35.9	729	9	CC543266	CC543266 CH240_424
	37	46.6	33.0	755	6	CB946232	CB946232 AGENCOURT
	38	46.6	33.0	930	5	BU513490	BU513490 AGENCOURT
	39	46.4	32.9	335	2	BE769053	BE769053 PM4-FT002
	40	46.4	32.9	1500	3	AK089916	AK089916 Mus muscu
	41	46	32.6	1047	4	BM925551	BM925551 AGENCOURT
	42	45	31.9	303	6	CA535795	CA535795 C0224B10-
	43	45	31.9	351	6	CF269885	CF269885 OKST Rat
	44	45	31.9	443	6	CA536077	CA536077 C0228H03-
	45	45	31.9	529	6	CB545374	CB545374 AMGNNUC:C

ALIGNMENTS

RESULT 1
AW976322/c
LOCUS AW976322 687 bp mRNA linear EST 02-JUN-2000
DEFINITION EST388431 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
ACCESSION AW976322
VERSION AW976322.1 GI:8167548
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 359
Seq primer: Forward.
FEATURES Location/Qualifiers
source 1. .687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSKm"
ORIGIN

Query Match 64.8%; Score 91.4; DB 2; Length 687;
Best Local Similarity 98.9%; Pred. No. 6.9e-15;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AATCAAAATCTGGTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AATCAAAATCTGTTTTTTTTTTTAACAAACATCTCAGTAATTACGCCAACATGTGAATAT 42

Qy         61 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCC 93
              |||||||||||||||||||||||||||||||||
Db         41 CACTGCCTCCTTTCTTCCTTTCAGAATATGGCC 9
```

```
RESULT 2
BE768971
LOCUS       BE768971                358 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  PM4-FT0023-020600-001-d09 FT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE768971
VERSION     BE768971.1  GI:10222629
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM4-FT0023-020
            600-001-d09&t3=2000-06-02&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 18
            High quality sequence stop: 358.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="FT0023"
                     /note="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             43.8%;  Score 61.8;  DB 2;  Length 358;
  Best Local Similarity   96.9%;  Pred. No. 1.1e-06;
  Matches   63;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         77 CCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 136
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 CCGTTAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAGCATGGCTG 99

Qy        137 CCCAG 141
              |||||
Db        100 CCCAG 104


RESULT 3
BX390237
LOCUS       BX390237                900 bp    mRNA    linear   EST 28-APR-2004
DEFINITION  BX390237 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YH04 5-PRIME, mRNA sequence.
ACCESSION   BX390237
VERSION     BX390237.2  GI:46834877
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30461423.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAG024ZA09_CS02273_1&c=5445.f
            .
FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI002YH04"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             43.8%;  Score 61.8;  DB 5;  Length 900;
  Best Local Similarity   90.4%;  Pred. No. 1.2e-06;
  Matches   66;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              || | ||  | |  ||||||||||||||||||||||||||||||||||||||||||||||
Db         42 CCCTCCTAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 101

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        102 CATGGCTGCCCAG 114


RESULT 4
BX495614
LOCUS       BX495614                370 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp779E0622_r1 779 (synonym: hncc1) Homo sapiens cDNA clone
            DKFZp779E0622_5', mRNA sequence.
ACCESSION   BX495614
VERSION     BX495614.1  GI:32010447
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 370)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
```

```
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Heinrich-
            Heine-University, Duesseldorf/Germany) within the cDNA sequencing
            consortium of the German Genome Project. No s1 sequence available.
            This clone (DKFZp779E0622) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
     source           1. .370
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="DKFZp779E0622"
                      /tissue_type="liver"
                      /dev_stage="fetal"
                      /lab_host="DH10B"
                      /clone_lib="779 (synonym: hncc1)"
                      /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN

  Query Match             43.4%;  Score 61.2;  DB 5;  Length 370;
  Best Local Similarity   92.5%;  Pred. No. 1.6e-06;
  Matches   74;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         63 CTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGTT-TTCTGTTTTATTACCAAGACATT 121
              ||||||||||||||||||||||||||||||||||   |||||||||||||||||| ||||
Db        124 CTGCCTCCTTTCTTCCTTTCAGAATATGGCCCAGAGCTTCTGTTTTATTACCAAGGCATT 183

Qy        122 AAAGTAGCATGGCTGCCCAG 141
              ||||| || ||||||||||||
Db        184 AAAGTNGCNTGGCTGCCCAG 203


RESULT 5
AI919501/c
LOCUS       AI919501                 257 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tp22b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188489 3'
            similar to SW:MTAP_HUMAN Q13126 5'-METHYLTHIOADENOSINE
            PHOSPHORYLASE ;, mRNA sequence.
ACCESSION   AI919501
VERSION     AI919501.1  GI:5639356
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 257)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1521   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 246.
FEATURES              Location/Qualifiers
     source           1. .257
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2188489"
                      /tissue_type="poorly differentiated adenocarcinoma with
                      signet ring cell features"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Gas4"
                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.69 kb. Life Technologies catalog #:
                      11549-011"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 1;  Length 257;
  Best Local Similarity   89.0%;  Pred. No. 2.8e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||
Db        135 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 76

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db         75 CATGGCTGCCCAG 63


RESULT 6
AA635142/c
LOCUS       AA635142                 491 bp    mRNA    linear   EST 21-OCT-1997
DEFINITION  af10e10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031274
            3' similar to TR:G847724 G847724 METHYLTHIOADENOSINE PHOSPHORYLASE.
            ;, mRNA sequence.
ACCESSION   AA635142
VERSION     AA635142.1  GI:2558356
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 289.
FEATURES              Location/Qualifiers
     source           1. .491
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1031274"
                      /sex="male"
                      /lab_host="DH10B"
                      /clone_lib="Soares_testis_NHT"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from mRNA obtained from Clontech
                      Laboratories, Inc., and primed with  a Not I - oligo(dT)
                      primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                      Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization to Cot5, and was
                      constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
```

```
  Query Match             42.7%;  Score 60.2;  DB 1;  Length 491;
  Best Local Similarity   89.0%;  Pred. No. 3.1e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 328

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        327 CATGGCTGCCCAG 315


RESULT 7
CD364939/c
LOCUS       CD364939                 570 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT2-bjn-i-17-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.
ACCESSION   CD364939
VERSION     CD364939.1  GI:31149029
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjn-i-17-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella  moi 10, 24 hours; Staph
                     aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
                     adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
                     hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
                     wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
                     The library was subtracted according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. The tissue
                     was provided by Dr. Gary W. Hunninghake of the University
                     of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT2
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 6;  Length 570;
  Best Local Similarity   89.0%;  Pred. No. 3.2e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 361

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        360 CATGGCTGCCCAG 348


RESULT 8
CN409515
LOCUS       CN409515                 612 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000600188932 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN409515
VERSION     CN409515.1  GI:47396639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 612   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .612
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, DMSO-treated H9 cell
                     line"
                     /clone_lib="GRN_PREHEP"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from DMSO-treated hES cell line H9 (p22) maintained in
                     feeder-free conditions"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 7;  Length 612;
  Best Local Similarity   89.0%;  Pred. No. 3.2e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 273

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        274 CATGGCTGCCCAG 286


RESULT 9
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BM784030
LOCUS       BM784030                681 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0062086 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-F01 5',
            mRNA sequence.
ACCESSION   BM784030
VERSION     BM784030.1  GI:19132262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 32  row: F  column: 01
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S6SNU620-32-F01"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Scattering floating"
                     /cell_line="SNU-620"
                     /lab_host="Top10F'"
                     /clone_lib="S6SNU620"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 4;  Length 681;
  Best Local Similarity   89.0%;  Pred. No. 3.3e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 355

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        356 CATGGCTGCCCAG 368


RESULT 10
CD364946/c
LOCUS       CD364946                684 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT2-bjn-k-07-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjn-k-07-0-UI 3', mRNA sequence.
ACCESSION   CD364946
VERSION     CD364946.1  GI:31149036
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjn-k-07-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella  moi 10, 24 hours; Staph
                     aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
                     adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
                     hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
                     wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
                     The library was subtracted according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. The tissue
                     was provided by Dr. Gary W. Hunninghake of the University
                     of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT2
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 6;  Length 684;
  Best Local Similarity   89.0%;  Pred. No. 3.3e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 361

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        360 CATGGCTGCCCAG 348
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RESULT 11
BF981023
LOCUS       BF981023                819 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  602310222F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4401533 5',
            mRNA sequence.
ACCESSION   BF981023
VERSION     BF981023.1  GI:12383835
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10108  row: k  column: 06
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4401533"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 2;  Length 819;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||
Db         99 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 158

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        159 CATGGCTGCCCAG 171


RESULT 12
AL048242
LOCUS       AL048242                836 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp586O1023_r1 586 (synonym: hute1) Homo sapiens cDNA clone
            DKFZp586O1023, mRNA sequence.
ACCESSION   AL048242
VERSION     AL048242.1  GI:4729075
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Ansorge, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone (DKFZp586O1023) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp586O1023"
                     /tissue_type="uterus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="586 (synonym: hute1)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 1;  Length 836;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||   |  | |  ||||||||||||||||||||||||||||||||||||||||||||
Db        305 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 364

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        365 CATGGCTGCCCAG 377


RESULT 13
BG574734
LOCUS       BG574734                836 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602596770F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705673 5',
            mRNA sequence.
ACCESSION   BG574734
VERSION     BG574734.1  GI:13582387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10572  row: k  column: 18
            High quality sequence stop: 680.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4705673"
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                /tissue_type="mammary adenocarcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_87"
                /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 1.383 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 4;  Length 836;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 65

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db         66 CATGGCTGCCCAG 78


RESULT 14
BX371508/c
LOCUS       BX371508                903 bp    mRNA    linear   EST 26-APR-2004
DEFINITION  BX371508 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YH04 3-PRIME, mRNA sequence.
ACCESSION   BX371508
VERSION     BX371508.1  GI:30448046
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI016ZH07_CS01496_1&c=5445.f

FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI002YH04"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 5;  Length 903;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 557

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        556 CATGGCTGCCCAG 544


RESULT 15
BX350035/c
LOCUS       BX350035                911 bp    mRNA    linear   EST 08-APR-2004
DEFINITION  BX350035 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YH06 3-PRIME, mRNA sequence.
ACCESSION   BX350035
VERSION     BX350035.2  GI:46307119
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 5, 2003 this sequence version replaced gi:30377483.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            340.r
            There is a virtual cDNA representing this cluster. For more
            information about this cluster and the virtual cDNA, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI016ZB08_CS01498_2&c=340.r.
FEATURES             Location/Qualifiers
     source          1. .911
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI002YH06"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             42.7%;  Score 60.2;  DB 5;  Length 911;
  Best Local Similarity   89.0%;  Pred. No. 3.4e-06;
  Matches   65;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         69 CCTTTCTTCCTTTCAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 128
              |||    |  | |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CCTCCATAACCTGAAGAATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAAAGTAG 550

Qy        129 CATGGCTGCCCAG 141
              |||||||||||||
Db        549 CATGGCTGCCCAG 537


Search completed: February  1, 2005, 14:58:28
Job time : 1589.32 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 219.128 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
Sequence: 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	383	9	AH013410S8	L42634 Homo sapien
2	39	100.0	499	6	AR425810	AR425810 Sequence
3	39	100.0	499	6	AX986504	AX986504 Sequence
4	39	100.0	499	6	BD121363	BD121363 EST and e
5	39	100.0	852	9	CR541670	CR541670 Homo sapi
6	39	100.0	870	6	AX826996	AX826996 Sequence
7	39	100.0	1021	9	L40432	L40432 Homo sapien
8	39	100.0	1890	9	BC026106	BC026106 Homo sapi
9	39	100.0	2269	9	HSU22233	U22233 Human methy
10	39	100.0	2763	6	AR059583	AR059583 Sequence
11	39	100.0	2763	6	I28320	I28320 Sequence 1
12	39	100.0	2763	6	AR473576	AR473576 Sequence
13	39	100.0	2763	6	AR474046	AR474046 Sequence
14	39	100.0	3083	6	AR144466	AR144466 Sequence
15	39	100.0	3083	6	AR342446	AR342446 Sequence
16	39	100.0	168656	9	AL359922	AL359922 Human DNA
17	39	100.0	250000	9	AB060808	AB060808 Homo sapi
18	36	92.3	849	9	CR541710	CR541710 Homo sapi
19	32.6	83.6	1055	10	AB056100	AB056100 Mus muscu
20	32.6	83.6	2565	10	BC003858	BC003858 Mus muscu
c 21	32.6	83.6	194025	10	AL831719	AL831719 Mouse DNA
c 22	32.6	83.6	225782	2	AC109529	AC109529 Rattus no
c 23	32.6	83.6	287775	2	AC108638	AC108638 Rattus no
c 24	32	82.1	32	6	AR342445	AR342445 Sequence
c 25	24.8	63.6	212886	2	AC093946	AC093946 Rattus no
26	24.8	63.6	234471	2	AC121424	AC121424 Rattus no
27	24.6	63.1	122176	2	AL358233	AL358233 Homo sapi
28	24.6	63.1	152224	2	AC007933	AC007933 Homo sapi
29	24.6	63.1	155044	2	CR450771	CR450771 Danio rer
c 30	24.6	63.1	175046	2	AC022728	AC022728 Homo sapi
c 31	24.6	63.1	188983	2	BX511222	BX511222 Danio rer
c 32	24.6	63.1	193774	9	AL445183	AL445183 Human DNA
c 33	24.6	63.1	232296	2	CR392026	CR392026 Danio rer
34	24.4	62.6	40011	9	AC026364	AC026364 Homo sapi
c 35	24.4	62.6	177594	9	AC026368	AC026368 Homo sapi
36	24.4	62.6	194919	2	AC127899	AC127899 Homo sapi
c 37	24.2	62.1	221189	2	AC131130	AC131130 Rattus no
c 38	24.2	62.1	228972	2	AC139930	AC139930 Rattus no
c 39	24.2	62.1	233619	2	AC128426	AC128426 Rattus no
40	24.2	62.1	248032	2	AC105801	AC105801 Rattus no
c 41	24.2	62.1	250876	2	AC097179	AC097179 Rattus no
c 42	24.2	62.1	324359	2	AC127115	AC127115 Rattus no
43	24	61.5	117406	9	AC010792	AC010792 Homo sapi
c 44	24	61.5	177152	9	BX544879	BX544879 Human DNA
45	24	61.5	201397	9	AC091628	AC091628 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AH013410S8 383 bp DNA linear PRI 01-DEC-2003
DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 8 and partial cds.
ACCESSION L42634
VERSION L42634.1 GI:38570314
KEYWORDS .
SEGMENT 8 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 383)
AUTHORS Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.
TITLE Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
MEDLINE 96234115
PUBMED 8650244
FEATURES Location/Qualifiers
source 1. .383
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22-p21"
/clone="1"
/tissue_type="placenta"
gene order(L42627.1:1. .199,L42628.1:1. .316,L42629.1:1. .190, L42630.1:1. .280,L42631.1:1. .441,L42632.1:1. .567, L42633.1:1. .303,1. .383)
/gene="MTAP"
mRNA join(L42627.1:1. .151,L42628.1:200. .286,L42629.1:124. .182, L42630.1:49. .216,L42631.1:178. .280,L42632.1:64. .303, L42633.1:76. .198,138. .>383)
/gene="MTAP"
/product="methylthioadenosine phosphorylase"
CDS join(L42627.1:119. .151,L42628.1:200. .286, L42629.1:124. .182,L42630.1:49. .216,L42631.1:178. .280, L42632.1:64. .303,L42633.1:76. .198,138. .176)

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                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
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                     /note="putative"
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Db        138 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 176


RESULT 2
AR425810
LOCUS       AR425810                499 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17307 from patent US 6639063.
ACCESSION   AR425810
VERSION     AR425810.1  GI:40180920
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 17307 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.00065;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        359 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 397


RESULT 3
AX986504
LOCUS       AX986504                499 bp    DNA     linear   PAT 15-JAN-2004
DEFINITION  Sequence 17307 from Patent EP1104808.
ACCESSION   AX986504
VERSION     AX986504.1  GI:40992644
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
  TITLE     ESTs and encoded human proteins
  JOURNAL   Patent: EP 1104808-A 17307 06-JUN-2001;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .499
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.00065;
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Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        359 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 397


RESULT 4
BD121363
LOCUS       BD121363                499 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  EST and encoded human protein.
ACCESSION   BD121363
VERSION     BD121363.1  GI:23216273
KEYWORDS    JP 2002010789-A/13440.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
  TITLE     EST and encoded human protein
  JOURNAL   Patent: JP 2002010789-A 13440 15-JAN-2002;
            GENSET CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002010789-A/13440
            PD   15-JAN-2002
            PF   07-AUG-2000 JP 2000280989
            PR   05-AUG-1999 US    60/147499
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE  PI
             GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
            C12N15/00
            CC   EST and encoded human protein
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.00065;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        359 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 397


RESULT 5
CR541670
LOCUS       CR541670                852 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834G1127D for
            gene MTAP, methylthioadenosine phosphorylase; complete cds, incl.
            stopcodon.
ACCESSION   CR541670
VERSION     CR541670.1  GI:49456300
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 852)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 852)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834G1127D, ORFNo 3305
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834G1127D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned incl. stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence NM_002451 (GI:6006025) we found
            AA exchange(s) at position (first base of changed triplet):
            139(leu->met) 166(ile->val)
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES              Location/Qualifiers
     source           1. .852
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
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                      /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                      /lab_host="DH5Alpha"
                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene             1. .852
                      /gene="MTAP"
     CDS              1. .852
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                      /db_xref="GI:49456301"
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                      LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                      TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                      SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 9;  Length 852;
  Best Local Similarity  100.0%;  Pred. No. 0.00059;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
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Db        814 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 852


RESULT 6
AX826996
LOCUS       AX826996                 870 bp    DNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 1 from Patent WO03074083.
ACCESSION   AX826996
VERSION     AX826996.1  GI:39837205
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bloom,L.A., Boritzki,T.J., Kung,P.P., Ogden,R.C., Skalitzky,D.J.,
            Zehnder,L.R., Kuhn,L.A. and Meng,J.J.
  TITLE     Combination therapies for treating methylthioadenosine
            phosphorylase deficient cells
  JOURNAL   Patent: WO 03074083-A 1 12-SEP-2003;
            PFIZER INC. (US)
FEATURES              Location/Qualifiers
     source           1. .870
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                      /note="Cloned MTAP cDNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0.00059;
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              |||||||||||||||||||||||||||||||||||||||
Db        820 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 858


RESULT 7
L40432
LOCUS       L40432                   1021 bp    mRNA    linear   PRI 12-DEC-2000
DEFINITION  Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
            complete cds.
ACCESSION   L40432
VERSION     L40432.1  GI:11602391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Genomic cloning of methylthioadenosine phosphorylase: a purine
            metabolic enzyme deficient in multiple different cancers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
  MEDLINE   96234115
   PUBMED   8650244
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
            Research on Aging, and Department of Medicine, University of
            California at San Diego, La Jolla, CA 92093-0663, USA
COMMENT     GSDB:S:39613.
            [Flatfile retrieved from GSDB Thu Dec  7 15:18:48 2000].
FEATURES              Location/Qualifiers
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     CDS             111. .962
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                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 9;  Length 1021;
  Best Local Similarity   100.0%;  Pred. No. 0.00057;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        924 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 962


RESULT 8
BC026106
LOCUS       BC026106                1890 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone
            MGC:33067 IMAGE:4820938), complete cds.
ACCESSION   BC026106
VERSION     BC026106.1  GI:19913486
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1890)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1890)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 46 Row: h Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006025.
FEATURES             Location/Qualifiers
     source          1. .1890
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:33067 IMAGE:4820938"
                     /tissue_type="Brain, hippocampus"
                     /clone_lib="NIH_MGC_95"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
     gene            1. .1890
                     /gene="MTAP"
                     /note="synonyms: MSAP, c86fus"
                     /db_xref="LocusID:4507"
                     /db_xref="MIM:156540"
     CDS             96. .947
                     /gene="MTAP"
                     /codon_start=1
                     /product="5'-methylthioadenosine phosphorylase"
                     /protein_id="AAH26106.1"
                     /db_xref="GI:19913487"
                     /db_xref="LocusID:4507"
                     /db_xref="MIM:156540"
                     /translation="MASGTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCILLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 9;  Length 1890;
  Best Local Similarity   100.0%;  Pred. No. 0.00051;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        909 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 947


RESULT 9
HSU22233
LOCUS       HSU22233                2269 bp    mRNA    linear   PRI 25-NOV-1995
DEFINITION  Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.
ACCESSION   U22233
VERSION     U22233.1  GI:847723
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2269)
  AUTHORS   Olopade,O.I., Pomykala,H.M., Hagos,F., Sveen,L.W., Espinosa,R. III,
            Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and
            Bohlander,S.K.
  TITLE     Construction of a 2.8-megabase yeast artificial chromosome contig
```

```
            and cloning of the human methylthioadenosine phosphorylase gene
            from the tumor suppressor region on 9p21
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
  MEDLINE   95327672
   PUBMED   7604019
REFERENCE   2  (bases 1 to 2269)
  AUTHORS   Olopade,O.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,
            University of Chicago Pritzker School of Medicine, 5841 S. Maryland
            Avenue, Chicago, IL 60637-1470, USA
FEATURES             Location/Qualifiers
     source          1. .2269
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p21"
                     /clone="18-11 cDNA"
                     /sex="male"
                     /cell_line="primary culture"
                     /cell_type="fibroblast"
                     /tissue_type="epidermis"
     gene            1. .2269
                     /gene="MTAP"
     CDS             122. .973
                     /gene="MTAP"
                     /codon_start=1
                     /product="methylthioadenosine phosphorylase"
                     /protein_id="AAA81646.1"
                     /db_xref="GI:847724"
                     /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCILLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
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                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 9;  Length 2269;
  Best Local Similarity  100.0%;  Pred. No. 0.0005;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||
Db        935 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 973


RESULT 10
AR059583
LOCUS       AR059583               2763 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5840505.
ACCESSION   AR059583
VERSION     AR059583.1  GI:5986033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
  TITLE     Method for inhibiting adenylosuccinate synthetase activity in
            methylthioadenosine phosphorylase deficient cells
  JOURNAL   Patent: US 5840505-A 1 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 6;  Length 2763;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 11
I28320
LOCUS       I28320                 2763 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571510.
ACCESSION   I28320
VERSION     I28320.1  GI:1819096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Nobori,T. and Carson,D.A.
  TITLE     Method for selective methionine starvation of malignant cells in
            mammals
  JOURNAL   Patent: US 5571510-A 1 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 6;  Length 2763;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 12
AR473576
LOCUS       AR473576               2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689561.
ACCESSION   AR473576
VERSION     AR473576.1  GI:42711901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Tumor suppressor gene and methods for detection of cancer,
            monitoring of tumor progression and cancer treatment
  JOURNAL   Patent: US 6689561-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 6;  Length 2763;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 13
AR474046
LOCUS       AR474046               2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689864.
ACCESSION   AR474046
VERSION     AR474046.1  GI:42712799
KEYWORDS    .
SOURCE      Unknown.
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Cyclin dependent kinase 4 inhibitor
  JOURNAL   Patent: US 6689864-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 0.00048;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 14
AR144466
LOCUS       AR144466               3083 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6210917.
ACCESSION   AR144466
VERSION     AR144466.1  GI:15106333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A. and Carrera,C.J.
  TITLE     Method for suppressing multiple drug resistance in cancer cells
  JOURNAL   Patent: US 6210917-A 1 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .3083
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 6;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 0.00047;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 15
AR342446
LOCUS       AR342446               3083 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 25 from patent US 6576420.
ACCESSION   AR342446
VERSION     AR342446.1  GI:33737456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A., Schmid,M. and Carrera,C.J.
  TITLE     Method for early diagnosis of, and determination of prognosis in,
            cancer
  JOURNAL   Patent: US 6576420-A 25 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .3083
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 6;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 0.00047;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


Search completed: February  1, 2005, 13:25:58
Job time : 221.128 secs
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GenCore version 5.1.6

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Run on: February 1, 2005, 10:46:43 ; Search time 51.1826 Seconds
(without alignments)
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Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	39	100.0	603	6	ABQ59540	Abq59540 Human col
	2	39	100.0	870	10	ADC37133	Adc37133 Cloned me
	3	39	100.0	1437	4	AAH33683	Aah33683 Human col
	4	39	100.0	2197	10	ADC30327	Adc30327 Human nov
	5	39	100.0	2763	2	AAT15167	Aat15167 Methylthi
	6	39	100.0	2763	2	AAQ92813	Aaq92813 Human MTA
	7	39	100.0	2763	2	AAT85305	Aat85305 Human met
	8	39	100.0	2763	2	AAZ00866	Aaz00866 Human MTA
	9	39	100.0	2763	5	AAF86091	Aaf86091 Methylthi
	10	39	100.0	2763	10	AAD64097	Aad64097 Human met
	11	39	100.0	2784	2	AAQ99202	Aaq99202 Pseudomon
	12	39	100.0	3083	2	AAX58284	Aax58284 Human met
	13	39	100.0	3083	8	ABX10818	Abx10818 DNA encod
c	14	32	82.1	32	3	AAZ35375	Aaz35375 Methylthi
c	15	23	59.0	554	6	ABN87814	Abn87814 Human ova
c	16	23	59.0	554	8	ABX92240	Abx92240 Human ova
c	17	22.6	57.9	168575	4	AAH21613	Aah21613 Human hyp
	18	22	56.4	22	3	AAZ35354	Aaz35354 Sense pri
c	19	21.8	55.9	110000	6	ABA90521_05	Continuation (6 of
	20	21.6	55.4	302250	6	ABL67703	Abl67703 Oesophagu
	21	21.4	54.9	577	10	ADF74440	Adf74440 Murine ma
c	22	21.4	54.9	1062	6	ABZ13834	Abz13834 Arabidops
	23	21.4	54.9	1107	2	AAT76896	Aat76896 Brassica
	24	21.4	54.9	1120	2	AAV58304	Aav58304 Brassica
	25	21.4	54.9	1120	3	AAC61419	Aac61419 Genomic D
	26	21.4	54.9	1389	10	ADF18054	Adf18054 Mouse mat
c	27	21.4	54.9	1390	10	ADB31856	Adb31856 DNA encod
c	28	21.4	54.9	1390	12	ADO02262	Ado02262 Thalecres
c	29	21.4	54.9	1484	3	AAC47412	Aac47412 Arabidops
c	30	21.4	54.9	1487	3	AAC36225	Aac36225 Arabidops
	31	21.4	54.9	1790	10	ADF18052	Adf18052 cDNA enco
	32	21.4	54.9	1790	10	ADF74446	Adf74446 Full leng
	33	21.4	54.9	1790	12	ADI53689	Adi53689 Murine ma
	34	21.4	54.9	2421	2	AAT30867	Aat30867 80 kD pro
	35	21.4	54.9	2421	2	AAT85373	Aat85373 Tetrahyme
	36	21.4	54.9	2746	11	ADM03683	Adm03683 Human cDN
	37	21.4	54.9	3559	11	ADM01917	Adm01917 Human cDN
	38	21.4	54.9	9881	6	ABL54354	Abl54354 Chemicall
	39	21.4	54.9	11847	4	ABL29442	Abl29442 Drosophil
	40	21.4	54.9	11847	4	AAS57196	Aas57196 DNA encod
	41	21.4	54.9	11847	10	ADC35935	Adc35935 Drosophil
c	42	21.4	54.9	13427	6	ABL33927	Abl33927 Human imm
	43	21.4	54.9	18817	6	ABL34494	Abl34494 Human met
	44	21.4	54.9	18817	6	ABL70161	Abl70161 Chemicall
	45	21.4	54.9	60940	9	ADA02582	Ada02582 Human REL

ALIGNMENTS

RESULT 1
ABQ59540/c
ID ABQ59540 standard; cDNA; 603 BP.
XX
AC ABQ59540;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:3235.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiaglingam A, Lewis ME;
XX
DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which

```
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists
XX
SQ   Sequence 603 BP; 159 A; 119 C; 110 G; 206 T; 0 U; 9 Other;

  Query Match             100.0%;  Score 39;  DB 6;  Length 603;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        432 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 394


RESULT 2
ADC37133
ID   ADC37133 standard; cDNA; 870 BP.
XX
AC   ADC37133;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Cloned methylthioadenosine phosphorylase, MTAP, cDNA.
XX
KW   combination therapy; methylthioadenosine phosphorylase; MTAP; inhibitor;
KW   glycinamide ribonucleotide formyltransferase; GARFT;
KW   aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW   anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW   glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW   pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX
OS   Unidentified.
XX
PN   WO2003074083-A1.
XX
PD   12-SEP-2003.
XX
PF   17-FEB-2003; 2003WO-IB000615.
XX
PR   04-MAR-2002; 2002US-0361645P.
PR   09-DEC-2002; 2002US-0432275P.
XX
PA   (PFIZ ) PFIZER INC.
XX
PI   Bloom LA,  Boritzki TJ,  Kung P,  Ogden RC,  Skalitzky DJ;
PI   Zehnder LR,  Kuhn LA,  Meng JJ;
XX
DR   WPI; 2003-748252/70.
XX
PT   Selectively killing methylthioadenosine phosphorylase deficient cells
PT   used for treating cell proliferative disorders comprises administering
PT   glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX
PS   Example 3B; Page 182-183; 189pp; English.
XX
CC   This invention relates to novel combination therapies that selectively
CC   kill methylthioadenosine phosphorylase (MTAP) deficient cells. The
CC   combination therapies comprise administering an inhibitor of glycinamide
CC   ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC   ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC   toxicity agent during and after administration of the inhibitor. The
CC   combination therapies can be used for selectively killing MTAP deficient
CC   cells, and for treating cell proliferative disorders e.g. lung cancer,
CC   leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC   prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC   The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC   MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC   dose of the inhibitor. This polynucleotide sequence represents the cloned
CC   MTAP cDNA of the invention.
XX
SQ   Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 39;  DB 10;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        820 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 858


RESULT 3
AAH33683
ID   AAH33683 standard; cDNA; 1437 BP.
XX
AC   AAH33683;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:739.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 9; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US026524.
XX
PR   29-SEP-1999;   99US-0157137P.
PR   03-NOV-1999;   99US-0163280P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   P-PSDB; AAG74252.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS   Claim 1; Page 2728-2729; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX
SQ   Sequence 1437 BP; 501 A; 202 C; 262 G; 460 T; 0 U; 12 Other;

  Query Match             100.0%;  Score 39;  DB 4;  Length 1437;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-05;
```

```
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        120 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 158


RESULT 4
ADC30327
ID   ADC30327 standard; cDNA; 2197 BP.
XX
AC   ADC30327;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human novel cDNA sequence, SEQ ID NO:409.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; chromosome 3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003029271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY,  Zhang J,  Ren F,  Xue AJ,  Zhao QA,  Wang J,  Wehrman T;
PI   Zhou P,  Ghosh M,  Wang D,  Ma Y,  Asundi V,  Wang Z,  Weng G;
PI   Haley-Vicente D,  Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC31298.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet
PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 409; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
CC   recombinant production of a polypeptide of the invention; an antibody
CC   against a polypeptide of the invention; a method of detecting
CC   polynucleotides or polypeptides of the invention; and methods of
CC   identifying a compound which binds to a polypeptide of the invention. The
CC   invention further discloses methods of peventing, treating or
CC   ameliorating a medical condition; kits comprising polynucleotide probes
CC   and/or monoclonal antibodies for carrying out the methods of the
CC   invention; methods for the identification of compounds that modulate the
CC   expression or activity of the polynucleotide and/or polypeptide; and 767
CC   contig sequences corresponding to the cDNA sequences of the invention
CC   (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC   -ADC33394). The nucleic acids and polypeptides of the invention are
CC   useful in diagnostics, drug screening, forensics, gene mapping, in the
CC   identification of mutations responsible for genetic disorders or other
CC   traits, for assessing biodiversity, and in producing many other types of
CC   data and products dependent on DNA and amino acid sequences. They are
CC   also used for treating diseases such as Parkinson's disease, Alzheimer's
CC   disease and other neurodegenerative diseases, anaemia, platelet
CC   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC   cancer. The nucleic acids may also be used as hybridisation probes or
CC   primers, and in the recombinant production of a protein. The polypeptides
CC   are also useful in generating antibodies, as molecular weight markers,
CC   and as food supplements. The present sequence represents a specifically
CC   claimed human cDNA sequence of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 39;  DB 10;  Length 2197;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        874 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 912


RESULT 5
AAT15167
ID   AAT15167 standard; DNA; 2763 BP.
XX
AC   AAT15167;
XX
DT   29-JUN-1996  (first entry)
XX
DE   Methylthioadenosine-phosphorylase gene.
XX
KW   Human; methylthioadenosine-phosphorylase; chromosome walking;
KW   interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW   cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW   melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW   non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW   antibody; imaging; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  b
FT   intron          422. .615
FT                   /*tag=  c
FT   exon            616. .720
FT                   /*tag=  d
FT   intron          721. .963
FT                   /*tag=  e
FT   exon            964. .1203
FT                   /*tag=  f
XX
PN   WO9528169-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;   95WO-US004655.
XX
PR   14-APR-1994;   94US-00227800.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 1995-373630/48.
XX
PT   Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT   useful for diagnosis, assessing predisposition and treatment of cancers.
XX
PS   Example 1; Page 96-101; 129pp; English.
XX
```

```
CC   The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC   at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC   tumour suppressor gene (AAT15157-58) is located between this gene and an
CC   interferon-alpha gene cluster, and has been isolated by chromosome
CC   walking. The CDK4I gene, probe and primer derivatives and the gene
CC   product may be used in diagnosis of cancer, particularly melanoma
CC   (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC   carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC   or in antitumour antisense oligonucleotide or ribozyme construction.
CC   Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 39;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 6
AAQ92813
ID   AAQ92813 standard; DNA; 2763 BP.
XX
AC   AAQ92813;
XX
DT   25-MAR-2003  (revised)
DT   05-DEC-1995  (first entry)
XX
DE   Human MTAse.
XX
KW   MTAse; methyladenosine-phosphatase; malignancy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  a
FT   exon            616. .720
FT                   /*tag=  b
FT   exon            964. .1203
FT                   /*tag=  c
FT   exon            1640. .1762
FT                   /*tag=  d
FT   exon            2272. .2310
FT                   /*tag=  e
XX
PN   WO9518233-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014920.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CIBA ) CIBA GEIGY CORP.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 1995-246398/32.
XX
PT   Detecting methyl:adenosine phosphatase in mammalian cells - by
PT   hybridisation with specific oligonucleotide for detecting malignancy,
PT   also new nucleic acid, expression vectors, derived polypeptide(s) and
PT   antibodies.
XX
PS   Claim 8; Page 34-35; 47pp; English.
XX
CC   A cosmid gene library constructed from human placenta DNA was screened
CC   using a MTAse cDNA probe to isolate a human MTAse genomic clone (sequence
CC   given in AAQ92813). Absence of MTAse from a cell is indicative of
CC   malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 39;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 7
AAT85305
ID   AAT85305 standard; DNA; 2763 BP.
XX
AC   AAT85305;
XX
DT   28-FEB-1998  (first entry)
XX
DE   Human methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   adenylsuccinate synthetase; lung cancer; glioma;
KW   acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  a
FT                   /number= 1
FT   intron          422. .615
FT                   /*tag=  b
FT                   /number= 1
FT   exon            616. .720
FT                   /*tag=  c
FT                   /number= 2
FT   intron          721. .963
FT                   /*tag=  d
FT                   /number= 2
FT   exon            964. .1203
FT                   /*tag=  e
FT                   /number= 3
XX
PN   WO9732994-A1.
XX
PD   12-SEP-1997.
XX
PF   27-JAN-1997;   97WO-US001193.
XX
PR   08-MAR-1996;   96US-00612542.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 1997-470550/43.
XX
PT   Inhibiting adenyl:succinate synthetase activity in methylthio:adenosine
PT   phosphorylase-deficient cells - by treatment with specific inhibitor,
PT   especially L-alanosine, useful for selective killing of MTAse deficient
PT   cancer cells.
XX
PS   Example 3; Page 25-26; 37pp; English.
XX
CC   This DNA sequence comprises human genomic DNA for methylthioadenosine
CC   phosphorylase (MTase), obtained from a cosmid gene library constructed
CC   from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC   method for inhibiting the activity adenylsuccinate synthetase (ASS) in
CC   mammalian cells deficient in MTAse activity involves: (a) determining
```

```
CC   that a population of cells obtained from a mammalian host is MTase
CC   deficient; and (b) administering an ASS inhibitor (preferably L-
CC   alanosine) to the host so that the MTase deficient host cells are
CC   depleted of AMP. The method is especially used to treat human MTAse-
CC   deficient primary tumour cells, specifically non-small cell lung cancer,
CC   acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC   MTAse catabolises methylthioadenosine to adenine for endogenous salvage
CC   incorporation into the intracellular AMP pool. The claimed method
CC   deprives the cells of substrate for de novo synthesis of AMP, resulting
CC   in selective killing of these cells. MTAse sequence-specific
CC   oligonuclotides can be used to detect the presence or absence of MTAse in
CC   malignant cell lines
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

  Query Match          100.0%;  Score 39;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 8
AAZ00866
ID   AAZ00866 standard; DNA; 2763 BP.
XX
AC   AAZ00866;
XX
DT   20-OCT-1999  (first entry)
XX
DE   Human MTAse DNA.
XX
KW   MTAse; methylthioadenosine phosphorylase; human; detection; active;
KW   catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            253. .421
FT                   /*tag=  a
FT                   /number= 1
FT                   /note= "Putative exon"
FT   intron          422. .615
FT                   /*tag=  b
FT                   /number= 1
FT                   /note= "putative intron"
FT   exon            616. .720
FT                   /*tag=  c
FT                   /number= 2
FT                   /note= "putative exon"
FT   intron          721. .963
FT                   /*tag=  d
FT                   /number= 2
FT                   /note= "putative intron"
FT   exon            964. .1203
FT                   /*tag=  e
FT                   /number= 3
FT                   /note= "putative exon"
XX
PN   US5942393-A.
XX
PD   24-AUG-1999.
XX
PF   18-DEC-1996;   96US-00772113.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Takabayashi K,  Carson DA,  Nobori T;
XX
DR   WPI; 1999-507775/42.
XX
PT   Detecting catalytically active and inactive methylthioadenosine
PT   phosphorylase (MTAse) in mammalian cells useful for identifying malignant
PT   cells which are suitable targets for methionine (MET) starvation therapy.
XX
PS   Claim 6; Fig 1; 14pp; English.
XX
CC   This invention describes a novel method for detecting catalytically
CC   active and inactive methylthioadenosine phosphorylase (MTAse) in
CC   mammalian cells, using oligonucleotide probes which hybridize to MTAse
CC   nucleic acid coding regions. Detection of MTAse encoding nucleic acid
CC   indicates the cell has catalytically active MTAse. The method is useful
CC   for detecting malignant cells with a deficient MTAse gene, useful for
CC   identifying malignant cells which are suitable targets for methionine
CC   (MET) starvation therapy. The new method is simple, efficient and
CC   successful at determining MTAse negative cells, unlike prior art
CC   techniques, which include analysis of catalytic activity in cell
CC   cultures, requiring a commercially unavailable radiochemical substrate,
CC   and immunoassays, using MTAse antibodies which are unable to be produced
CC   in sufficient quantities. Recombinant MTAse protein produced using the
CC   new polynucleotide and vector, allows greater and purer production of
CC   MTAse than prior art techniques (using the Rangione method) for isolating
CC   native MTAse. This sequence represents human MTAse encoding DNA which is
CC   used in the method of the invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match          100.0%;  Score 39;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 9
AAF86091
ID   AAF86091 standard; DNA; 2763 BP.
XX
AC   AAF86091;
XX
DT   06-JUL-2001  (first entry)
XX
DE   Methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW   cancer; ds.
XX
OS   Unidentified.
XX
PN   US6214571-B1.
XX
PD   10-APR-2001.
XX
PF   24-NOV-1998;   98US-00199137.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 2001-315458/33.
XX
PT   Inhibiting adenine succinate synthetase (ASS) activity in
PT   methylthioadenosine phosphorylase deficient cells of mammalian host
PT   involves administering ASS inhibitor which depletes adenosine 5'
PT   monophosphate in cells.
XX
PS   Disclosure; Fig 1; 17pp; English.
XX
```

```
CC   The present invention relates to inhibiting adenyl succinate synthetase
CC   (ASS) activity in methylthioadenosine phosphorylase (MTAse) deficient
CC   cells of mammalian host. The invention may be used as a treatment for
CC   cancer, especially breest and colon cancer
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 39;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 10
AAD64097
ID   AAD64097 standard; DNA; 2763 BP.
XX
AC   AAD64097;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human methylthioadenosine phosphorylase (MTAse) genomic DNA.
XX
KW   Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW   CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTAse;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  a
FT   intron          422. .615
FT                   /*tag=  b
FT   exon            616. .720
FT                   /*tag=  c
FT   intron          721. .963
FT                   /*tag=  d
FT   exon            964. .1203
FT                   /*tag=  e
XX
PN   US2003138928-A1.
XX
PD   24-JUL-2003.
XX
PF   18-JUL-2001; 2001US-00908671.
XX
PR   26-AUG-1997;   97US-00921954.
XX
PA   (CARS/) CARSON D A.
PA   (NOBO/) NOBORI T.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 2003-851737/79.
XX
PT   New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
PT   for preparing a composition for diagnosing or treating cancer.
XX
PS   Example 1; SEQ ID NO 14; 46pp; English.
XX
CC   The present invention relates to novel tumour suppressor genes, termed as
CC   cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC   proteins. The polynucleotides are useful for preparing a composition for
CC   diagnosing or treating cancer. Sequences of the invention are also useful
CC   in gene therapy. The present sequence is human methylthioadenosine
CC   phosphorylase (MTAse) genomic DNA used in the exemplification of the
CC   invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 39;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 11
AAQ99202
ID   AAQ99202 standard; DNA; 2784 BP.
XX
AC   AAQ99202;
XX
DT   07-MAR-1996  (first entry)
XX
DE   Pseudomonas putida methylthioadenosine-phosphorylase DNA.
XX
KW   Enzyme; MTAase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW   chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS   Pseudomonas putida.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2763
FT                   /*tag=  a
XX
PN   WO9517908-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014919.
XX
PR   29-DEC-1993;   93US-00176413.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Nobori T,  Carson DA;
XX
DR   WPI; 1995-246192/32.
XX
PT   Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT   negative tumour cells - used in chemotherapy of mammalian malignant
PT   cells.
XX
PS   Disclosure; Page 27-28; 46pp; English.
XX
CC   Antigenic peptides may be generated from this sequence encoding
CC   methyladenosine-phosphorylase, which are then used to generate antibodies
CC   specific for MTAse. The produced antibodies may be used in an immunoassay
CC   for the detection of MTase
XX
SQ   Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

  Query Match             100.0%;  Score 39;  DB 2;  Length 2784;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
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Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 12
AAX58284
ID   AAX58284 standard; DNA; 3083 BP.
XX
AC   AAX58284;
XX
DT   02-AUG-1999  (first entry)
XX
```

```
DE   Human methylthioadenosine phosphorylase genomic DNA.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             119. .2876
FT                   /*tag= a
FT                   /note= "contains introns"
FT   exon            119. .151
FT                   /*tag= b
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag= c
FT                   /number= 1
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FT                   /number= 2
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FT   exon            724. .782
FT                   /*tag= f
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag= g
FT                   /number= 3
FT   exon            899. .1067
FT                   /*tag= h
FT                   /number= 4
FT   intron          1068. .1377
FT                   /*tag= i
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FT   exon            1378. .1480
FT                   /*tag= j
FT                   /number= 5
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FT                   /number= 5
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FT                   /number= 6
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FT                   /*tag= m
FT                   /number= 6
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FT                   /number= 7
FT   intron          2549. .2837
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FT                   /*tag= p
FT                   /number= 8
XX
PN   WO9920791-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022557.
XX
PR   23-OCT-1997;   97US-00956657.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Cottam HB,  Nobori T,  Carrera CJ;
XX
DR   WPI; 1999-302753/25.
XX
PT   Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT   leukemia's.
XX
PS   Example 3; Page 42-44; 45pp; English.
XX
CC   This is the DNA sequence of a human methylthioadenosine phosphorylase
CC   (MTAse) genomic DNA clone that was isolated from a cosmid gene library
CC   using an MTAse cDNA probe. The encoded enzyme catabolises
CC   methylthioadenosine to adenine for endogenous salvage incorporation into
CC   the intracellular AMP pool. The invention relates to methods for treating
CC   and preventing the onset and maintenance of multiple drug resistance
CC   (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC   cells are depleted of AMP and ATP and are thus unable to supprt P-
CC   glycoprotein activity. One method obtains a population of target cells
CC   from a host and assays for loss of MTAse activity. MTAse deficient cells
CC   are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC   starves the cells of adenine and suppresses P-glycoprotein activity. The
CC   MTAse deficient host cells are preferably primary tumour cells comprising
CC   small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC   cells or urothelial tumor cells, preferably in humans. MTAse competent
CC   cells are also treated for MDR with purine synthesis inhibitors. MTAse
CC   competent and deficient cells are also treated for malignancy with other
CC   anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC   to detect the presence or absence of MTAse in malignant cell lines
XX
SQ   Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;

  Query Match             100.0%;  Score 39;  DB 2;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 13
ABX10818
ID   ABX10818 standard; DNA; 3083 BP.
XX
AC   ABX10818;
XX
DT   17-APR-2003  (first entry)
XX
DE   DNA encoding rat methylthioadenosine phosphorylase (MTAse).
XX
KW   Rat; methylthioadenosine phosphorylase; MTAse; detection;
KW   Rangione method; gene; ds.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   exon            119. .151
FT                   /*tag= a
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag= b
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag= a
FT                   /number= 2
FT   intron          537. .723
FT                   /*tag= b
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag= a
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag= b
FT                   /number= 3
FT   exon            899. .1066
FT                   /*tag= a
FT                   /number= 4
FT   intron          1067. .1377
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FT                   /*tag=  b
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FT   exon            1378. .1480
FT                   /*tag=  a
FT                   /number= 5
FT   intron          1481. .1763
FT                   /*tag=  b
FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag=  a
FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag=  b
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag=  a
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag=  b
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag=  a
FT                   /number= 8
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PN   US2002146695-A1.
XX
PD   10-OCT-2002.
XX
PF   09-FEB-2001; 2001US-00780114.
XX
PR   29-DEC-1993;   93US-00176855.
PR   02-JUN-1995;   95US-00459343.
PR   04-MAY-1998;   98US-00072914.
XX
PA   (NOBO/) NOBORI T.
PA   (CARS/) CARSON D A.
PA   (TAKA/) TAKABAYASHI K.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 2003-208976/20.
XX
PT   Detection of methylthioadenosine phosphorylase presence in mammalian
PT   cells, by adding to sample oligonucleotide probes capable of hybridizing
PT   to methylthioadenosine phosphorylase encoding nucleic acid.
XX
PS   Claim 7; Fig 1; 16pp; English.
XX
CC   The invention describes a method of detecting methylthioadenosine
CC   phosphorylase (MTAse) comprising adding oligonucleotide probes
CC   hybridisable to MTAse encoding nucleic acid to an assayable sample of
CC   cells, where the presence of the nucleic acid indicates the presence of
CC   the MTAse in a cell. The inventive method is simple and efficient in
CC   detecting the presence of MTAse in the mammalian cell. The availability
CC   of the recombinant MTAse enables the production of highly pure material
CC   with greater ease and in greater quantities than was obtained using
CC   Rangione method for the isolation and purification of native MTAse. This
CC   sequence encodes rat methylthioadenosine phosphorylase (MTAse)
XX
SQ   Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

  Query Match             100.0%;  Score 39;  DB 8;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 14
AAZ35375/c
ID   AAZ35375 standard; DNA; 32 BP.
XX
AC   AAZ35375;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Methylthioadenosine phosphorylase gene exons 5-8 antisense primer.
XX
KW   Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis;
KW   methylthioadenosine phosphorylase; MTAP; glioma; melanoma;
KW   primary lymphoid malignancy; non-small cell lung cancer;
KW   head and neck cancer; ovarian cancer; bladder cancer; chondrosarcoma;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967634-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013981.
XX
PR   23-JUN-1998;   98US-0090411P.
PR   17-JUN-1999;   99US-00335231.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Schmid M,  Carrera CJ;
XX
DR   WPI; 2000-126650/11.
XX
PT   Diagnosing and determining prognosis for cancer causitively associated
PT   with derangements of chromosome 9p21.
XX
PS   Claim 7; Page 16; 55pp; English.
XX
CC   This antisense primer is designed for the PCR amplification of exons 5-8
CC   of the human methylthioadenosine phosphorylase (MTAP) gene on chromosome
CC   9p21 (see AAZ35351). The primer is used, with a sense primer (see
CC   AAZ35374), in a PCR amplification (505 bp product) in step (a) of claimed
CC   methods for diagnosis of, and determining a prognosis for, cancer
CC   causatively associated with derangements of chromosome 9p21. Step (a) of
CC   these methods involves determining whether any portion of the 9p21
CC   chromosome including and telomeric to STS 3.21 is deleted, or whether any
CC   portion of the gene encoding MTAP is deleted. Step (b) involves
CC   determining whether any portion of 9p21 centromeric to STS 3.21 is
CC   deleted, or whether any portion of the gene coding for p16 is deleted.
CC   The results are indicative of a cancer at an early stage or advanced
CC   stage of tumour development. Primer pairs (see AAZ35354-75) are provided
CC   for use in the claimed methods, where the cancer is a glioma, primary
CC   lymphoid malignancy, non-small cell lung cancer, melanoma, head and neck
CC   cancer, ovarian cancer, bladder cancer or a chondrosarcoma (claimed)
XX
SQ   Sequence 32 BP; 13 A; 3 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             82.1%;  Score 32;  DB 3;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
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Db         32 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 1


RESULT 15
ABN87814/c
ID   ABN87814 standard; cDNA; 554 BP.
XX
AC   ABN87814;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human ovary specific nucleic acid SEQ ID NO:25.
XX
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KW Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP;
KW ovary specific gene; OSG; ovarian cancer; immune response; metastasis;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200240535-A2.
XX
PD 23-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US045011.
XX
PR 20-NOV-2000; 2000US-0252061P.
PR 27-NOV-2000; 2000US-0253257P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu C;
XX
DR WPI; 2002-471617/50.
XX
PT New ovary specific genes and proteins, useful as a vaccine for treating
PT patients with ovarian cancer, or for diagnosing and monitoring the
PT presence and metastases of ovarian cancer in a patient.
XX
PS Claim 1; Page 169; 260pp; English.
XX
CC ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA)
CC sequences, and ABB79297 to ABB79370 represent ovary specific protein
CC (OSP) sequences from the present invention. OSNA and OSP sequences have
CC cytostatic activity, and can be used in vaccine production and gene
CC therapy. An antibody that specifically binds to an OSP can be used for
CC treating a patient with ovarian cancer, particularly for inducing an
CC immune response against the ovarian cancer cell expressing the OSNA or
CC OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring
CC the presence and metastases of ovarian cancer in a patient
XX
SQ Sequence 554 BP; 182 A; 120 C; 136 G; 116 T; 0 U; 0 Other;

Query Match 59.0%; Score 23; DB 6; Length 554;
Best Local Similarity 83.9%; Pred. No. 48;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Search completed: February 1, 2005, 12:39:37
Job time : 52.1826 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 11.3915 Seconds
(without alignments)
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Perfect score: 39
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	39	100.0	2763	1	US-08-176-413-1	Sequence 1, Appli
3	39	100.0	2763	2	US-08-612-542B-1	Sequence 1, Appli
4	39	100.0	2763	2	US-08-772-113-1	Sequence 1, Appli
5	39	100.0	2763	3	US-09-199-137-1	Sequence 1, Appli
6	39	100.0	2763	4	US-08-227-800A-14	Sequence 14, Appl
7	39	100.0	2763	4	US-08-921-954-14	Sequence 14, Appl
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c 13	22.6	57.9	168575	4	US-09-426-290-1	Sequence 1, Appli
14	22	56.4	22	4	US-09-335-231-3	Sequence 3, Appli
15	21.4	54.9	1120	1	US-08-592-214A-21	Sequence 21, Appl
16	21.4	54.9	1120	3	US-09-149-976-21	Sequence 21, Appl
17	21.4	54.9	2421	3	US-08-851-843A-51	Sequence 51, Appl
18	21.4	54.9	2421	3	US-08-974-549A-218	Sequence 218, App
19	21.4	54.9	2421	3	US-08-854-050-51	Sequence 51, Appl
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21	21.4	54.9	2421	4	US-09-402-181B-218	Sequence 218, App
22	21.4	54.9	2421	4	US-09-721-456-218	Sequence 218, App
c 23	21	53.8	6617	4	US-09-976-594-268	Sequence 268, App
24	20.8	53.3	605	4	US-09-270-767-29748	Sequence 29748, A
25	20.8	53.3	1023	4	US-09-270-767-13726	Sequence 13726, A
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27	20.6	52.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
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34	20	51.3	799	3	US-09-095-485-1	Sequence 1, Appli
c 35	20	51.3	1106	5	PCT-US92-02977-5	Sequence 5, Appli
c 36	20	51.3	1106	5	PCT-US95-03032-4	Sequence 4, Appli
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38	20	51.3	1142	4	US-09-620-412C-113	Sequence 113, App
39	20	51.3	1142	4	US-09-598-419-113	Sequence 113, App
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45	20	51.3	2085	4	US-09-598-419-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17307
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17307

Query Match 100.0%; Score 39; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,413
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD2864
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-176-413-1

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  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
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RESULT 3
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
;  GENERAL INFORMATION:
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    APPLICANT:  No. 5840505ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    TITLE OF INVENTION:  METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
;    TITLE OF INVENTION:  ACTIVITY IN MALIGNANT METHYLTHIOADENOSINE PHOSPHORYLASE DEFICI
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,542B
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-612-542B-1

  Query Match             100.0%;  Score 39;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 4
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5942393ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Takabayashi, Kenji
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/772,113
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,855
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-772-113-1

  Query Match             100.0%;  Score 39;  DB 2;  Length 2763;
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  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 5
US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6214571ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,137
;      FILING DATE:  24-NOV-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-09-199-137-1

  Query Match             100.0%;  Score 39;  DB 3;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 6
US-08-227-800A-14
; Sequence 14, Application US/08227800A
; Patent No. 6689561
;  GENERAL INFORMATION:
;    APPLICANT:  CARSON, DENNIS A.
;    APPLICANT:  NOBORI, TSUTOMU
;    TITLE OF INVENTION:  TUMOR SUPPRESSOR GENE AND METHODS FOR
;    TITLE OF INVENTION:  DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANC
;    TITLE OF INVENTION:  TREATMENT
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,800A
;      FILING DATE:  14-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOWELLS, STACY L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/023001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Methylthioadenosine Phosphorylase (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-227-800A-14

  Query Match             100.0%;  Score 39;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 7
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
;  GENERAL INFORMATION:
;       APPLICANT: Carson, Dennis A.
;                  No. 6689864ori, Tsutomu
;       TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
;                           Detection of Cancer, Monitoring of Tumor Progression and
;                           Cancer Treatment
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
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;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/921,954
;             FILING DATE: 26-Aug-1997
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671A
;             FILING DATE: 18-Jul-2001
;             APPLICATION NUMBER: US 08/921,954
;             FILING DATE: 20-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Hinsch, Matthew E.
;             REGISTRATION NUMBER: 47,651
;             REFERENCE/DOCKET NUMBER: 02307O-104042US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;             NAME/KEY:  -
;             LOCATION:  1..2763
;             OTHER INFORMATION:  /note= "full-length
;             methylthioadenosine phosphorylase
;             (MTAse) genomic nucleotide sequence"
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  254..421
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  616..720
;       FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  964..1203
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

  Query Match             100.0%;  Score 39;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 8
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR SELECTIVE METHIONINE
;    TITLE OF INVENTION:  STARVATION OF MALIGNANT CELLS IN MAMMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14919
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-286
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14919-1

  Query Match             100.0%;  Score 39;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 9
PCT-US94-14920-1
; Sequence 1, Application PC/TUS9414920
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14920
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-287
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
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```
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     IMMEDIATE SOURCE:
;       CLONE:  methyladenosine phosphatase
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2763
PCT-US94-14920-1

  Query Match             100.0%;  Score 39;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2272 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2310


RESULT 10
US-08-956-657-1
; Sequence 1, Application US/08956657
; Patent No. 6210917
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6210917ori et al., Tsutomu
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/956,657
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/827,342
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Taylor, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/050001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3083 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-956-657-1

  Query Match             100.0%;  Score 39;  DB 3;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 8e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 11
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE:  02307O-108010US
;  CURRENT APPLICATION NUMBER: US/09/335,231
;  CURRENT FILING DATE:  1999-06-17
;  PRIOR APPLICATION NUMBER:  US 60/090,411
;  PRIOR FILING DATE:  1998-06-23
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-09-335-231-25

  Query Match             100.0%;  Score 39;  DB 4;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 8e-06;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 12
US-09-335-231-24/c
; Sequence 24, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
```

```
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE:  02307O-108010US
;  CURRENT APPLICATION NUMBER: US/09/335,231
;  CURRENT FILING DATE:  1999-06-17
;  PRIOR APPLICATION NUMBER:  US 60/090,411
;  PRIOR FILING DATE:  1998-06-23
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:anti-sense
;   OTHER INFORMATION: primer
US-09-335-231-24

  Query Match             82.1%;  Score 32;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.0018;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              ||||||||||||||||||||||||||||||||
Db         32 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 1


RESULT 13
US-09-426-290-1/c
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
;  APPLICANT: Berglind Ran Olafsdottir
;  APPLICANT: Jeffrey Gulcher
;  TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
;  FILE REFERENCE: 2345.2001-000
;  CURRENT APPLICATION NUMBER: US/09/426,290
;  CURRENT FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 168575
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (21181)...(21403)
;   NAME/KEY: CDS
;   LOCATION: (95252)...(95430)
;   NAME/KEY: CDS
;   LOCATION: (101753)...(101996)
;   NAME/KEY: CDS
;   LOCATION: (110324)...(110439)
;   NAME/KEY: CDS
;   LOCATION: (124058)...(124278)
;   NAME/KEY: CDS
;   LOCATION: (127009)...(127130)
;   NAME/KEY: CDS
;   LOCATION: (128910)...(129139)
US-09-426-290-1

  Query Match             57.9%;  Score 22.6;  DB 4;  Length 168575;
  Best Local Similarity   75.7%;  Pred. No. 22;
  Matches   28;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 ATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTA 38
              ||||||  || ||||||  |||  || ||||||  | ||
Db      60300 ATATGGTACATTTTTCTCTTTCTTTTCCAAGAAAGTA 60264


RESULT 14
US-09-335-231-3
; Sequence 3, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE:  02307O-108010US
;  CURRENT APPLICATION NUMBER: US/09/335,231
;  CURRENT FILING DATE:  1999-06-17
;  PRIOR APPLICATION NUMBER:  US 60/090,411
;  PRIOR FILING DATE:  1998-06-23
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:sense primer
US-09-335-231-3

  Query Match             56.4%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 AGTTTTCTGTTTTATTACCAAG 32
              ||||||||||||||||||||||
Db          1 AGTTTTCTGTTTTATTACCAAG 22


RESULT 15
US-08-592-214A-21
; Sequence 21, Application US/08592214A
; Patent No. 5811536
;  GENERAL INFORMATION:
;    APPLICANT:  Yanofsky, Martin F.
;    TITLE OF INVENTION:  Cauliflower Floral Meristem Identify
;    TITLE OF INVENTION:  Genes and Methods of Using Same
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/592,214A
;      FILING DATE:  26-JAN-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UD 1927
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1120 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
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;       NAME/KEY:  unsure
;       LOCATION:  389..393
;       OTHER INFORMATION:  /note= "N = one or more
;       OTHER INFORMATION:  nucleotides."
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  810..814
;       OTHER INFORMATION:  /note= "N = one or more
;       OTHER INFORMATION:  nucleotides."
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  1118..1120
;       OTHER INFORMATION:  /note= "N = one or more
;       OTHER INFORMATION:  nucleotides."
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..1120
;       OTHER INFORMATION:  /note= "sequence = Brassica
;       OTHER INFORMATION:  oleracea CAL gene"
US-08-592-214A-21

  Query Match             54.9%;  Score 21.4;  DB 1;  Length 1120;
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  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

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Search completed: February  1, 2005, 15:01:04
Job time : 14.3915 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 53.6349 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
Sequence: 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	39	100.0	603	11	US-09-969-034-3235	Sequence 3235, Ap
	2	39	100.0	870	16	US-10-367-366-1	Sequence 1, Appli
	3	39	100.0	1437	15	US-10-106-698-749	Sequence 749, App
	4	39	100.0	2269	18	US-10-779-476-2	Sequence 2, Appli
	5	39	100.0	2763	10	US-09-908-671-14	Sequence 14, Appl
	6	39	100.0	3083	9	US-09-780-114-1	Sequence 1, Appli
	7	39	100.0	3083	15	US-10-326-681-25	Sequence 25, Appl
c	8	32	82.1	32	15	US-10-326-681-24	Sequence 24, Appl
c	9	24	61.5	678	13	US-10-027-632-29328	Sequence 29328, A
c	10	24	61.5	678	13	US-10-027-632-29329	Sequence 29329, A
c	11	24	61.5	678	15	US-10-027-632-29328	Sequence 29328, A
c	12	24	61.5	678	15	US-10-027-632-29329	Sequence 29329, A
c	13	24	61.5	808	13	US-10-027-632-31882	Sequence 31882, A
c	14	24	61.5	808	15	US-10-027-632-31882	Sequence 31882, A
c	15	23	59.0	554	15	US-10-076-747-54	Sequence 54, Appl
c	16	23	59.0	554	16	US-10-001-885-25	Sequence 25, Appl
c	17	22.6	57.9	1213	13	US-10-027-632-123022	Sequence 123022,
c	18	22.6	57.9	1213	13	US-10-027-632-123023	Sequence 123023,
c	19	22.6	57.9	1213	15	US-10-027-632-123022	Sequence 123022,
c	20	22.6	57.9	1213	15	US-10-027-632-123023	Sequence 123023,
c	21	22.6	57.9	168575	15	US-10-178-194-1	Sequence 1, Appli
	22	22	56.4	22	15	US-10-326-681-3	Sequence 3, Appli
	23	22	56.4	643	13	US-10-027-632-150817	Sequence 150817,
	24	22	56.4	643	15	US-10-027-632-150817	Sequence 150817,
	25	21.8	55.9	622	13	US-10-027-632-219425	Sequence 219425,
	26	21.8	55.9	622	15	US-10-027-632-219425	Sequence 219425,
c	27	21.8	55.9	1603	13	US-10-027-632-97331	Sequence 97331, A
c	28	21.8	55.9	1603	13	US-10-027-632-97332	Sequence 97332, A
c	29	21.8	55.9	1603	15	US-10-027-632-97331	Sequence 97331, A
c	30	21.8	55.9	1603	15	US-10-027-632-97332	Sequence 97332, A
	31	21.6	55.4	429	16	US-10-424-599-48727	Sequence 48727, A
c	32	21.6	55.4	2890	13	US-10-027-632-256650	Sequence 256650,
c	33	21.6	55.4	2890	13	US-10-027-632-256651	Sequence 256651,
c	34	21.6	55.4	2890	15	US-10-027-632-256650	Sequence 256650,
c	35	21.6	55.4	2890	15	US-10-027-632-256651	Sequence 256651,
	36	21.6	55.4	49088	13	US-10-087-192-13	Sequence 13, Appl
	37	21.6	55.4	56773	18	US-10-331-053-47	Sequence 47, Appl
c	38	21.6	55.4	194049	13	US-10-087-192-1495	Sequence 1495, Ap
	39	21.6	55.4	302250	9	US-09-962-832-154	Sequence 154, App
	40	21.4	54.9	577	15	US-10-409-643-10	Sequence 10, Appl
	41	21.4	54.9	689	13	US-10-027-632-244523	Sequence 244523,
	42	21.4	54.9	689	15	US-10-027-632-244523	Sequence 244523,
c	43	21.4	54.9	1062	9	US-09-938-842A-1639	Sequence 1639, Ap
c	44	21.4	54.9	1062	11	US-09-938-842A-1639	Sequence 1639, Ap
	45	21.4	54.9	1240	16	US-10-425-114-7600	Sequence 7600, Ap

ALIGNMENTS

RESULT 1
US-09-969-034-3235/c
; Sequence 3235, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3235
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 492, 497, 506, 527, 542, 544, 573, 576, 597
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235

Query Match 100.0%; Score 39; DB 11; Length 603;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
;  APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
;  APPLICANT:  Bloom, Laura  A
;  APPLICANT:  Kuhn, Leslie
;  APPLICANT:  Meng, Jerry Jialun
;  APPLICANT:  Kung, Pei-Pei
;  APPLICANT:  Zehnder, Luke
;  APPLICANT:  Boritzki, Theodore  J.
;  APPLICANT:  Ogden, Richard
;  APPLICANT:  Skalitzky , Donald
;  TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
;  TITLE OF INVENTION:  Phosphorylase Deficient Cells
;  FILE REFERENCE: PC19080A (AG110-01)
;  CURRENT APPLICATION NUMBER: US/10/367,366
;  CURRENT FILING DATE:  2003-02-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

  Query Match             100.0%;  Score 39;  DB 16;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 8e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
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RESULT 3
US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-106-698-749

  Query Match             100.0%;  Score 39;  DB 15;  Length 1437;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
;  APPLICANT: Salmedix, Inc.
;  APPLICANT:  Leoni,Lorenzo M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
;  TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
;  FILE REFERENCE: 076936-0307942
;  CURRENT APPLICATION NUMBER: US/10/779,476
;  CURRENT FILING DATE:  2004-02-13
;  PRIOR APPLICATION NUMBER: 60/447,888
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: 60/460,715
;  PRIOR FILING DATE: 2004-04-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-779-476-2

  Query Match             100.0%;  Score 39;  DB 18;  Length 2269;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||
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RESULT 5
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
;   GENERAL INFORMATION:
;        APPLICANT: CARSON, DENNIS A.
;                   NOBORI, TSUTOMU
;        TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
;                            DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
;                            TREATMENT
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: California
;             COUNTRY: US
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671
;             FILING DATE: 18-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/227,800
;             FILING DATE: 14-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HOWELLS, STACY L.
;             REGISTRATION NUMBER: 34,842
;             REFERENCE/DOCKET NUMBER: 07340/023001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
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;            TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 2763 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        IMMEDIATE SOURCE:
;            CLONE: Methylthioadenosine Phosphorylase (genomic)
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..2763
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

  Query Match             100.0%;  Score 39;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
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RESULT 6
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020146695A1ori, Tsutomu
;                   Carson, Dennis A.
;                   Takabayashi, Kenji
;        TITLE OF INVENTION: Method for Detection of the Presence or
;                            Absence of Methylthioadenosine Phosphorylase
;                            (MTAse) in a
;                            Cell Sample by Detection of the Presence or Absence
;        NUMBER OF SEQUENCES: 1
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/780,114
;            FILING DATE: 09-Feb-2001
;            CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/072,914
;            FILING DATE: 04-May-1998
;            APPLICATION NUMBER: US 08/176,855
;            FILING DATE: 29-DEC-1993
;            APPLICATION NUMBER: US 08/459,343
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 08/827,342
;            FILING DATE: 26-MAR-1997
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Bastian, Kevin L.
;            REGISTRATION NUMBER: 34,774
;            REFERENCE/DOCKET NUMBER: 023070-103030US
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 3083 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..3083
;            OTHER INFORMATION:  /note= "rat methylthioadenosine
;            phosphorylase (MTAse)"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  119..151
;            OTHER INFORMATION:  /note= "exon 1"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  450..536
;            OTHER INFORMATION:  /note= "exon 2"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  724..782
;            OTHER INFORMATION:  /note= "exon 3"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  899..1066
;            OTHER INFORMATION:  /note= "exon 4"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1378..1480
;            OTHER INFORMATION:  /note= "exon 5"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1764..1953
;            OTHER INFORMATION:  /note= "exon 6"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2426..2548
;            OTHER INFORMATION:  /note= "exon 7"
;        FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2838..2876
;            OTHER INFORMATION:  /note= "exon 8"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

  Query Match             100.0%;  Score 39;  DB 9;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 7
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; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE: 023070-108010US
;  CURRENT APPLICATION NUMBER: US/10/326,681
;  CURRENT FILING DATE:  2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/090,411
;  PRIOR FILING DATE: 1998-06-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-10-326-681-25

  Query Match             100.0%;  Score 39;  DB 15;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db       2838 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 2876


RESULT 8
US-10-326-681-24/c
; Sequence 24, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE: 02307O-108010US
;  CURRENT APPLICATION NUMBER: US/10/326,681
;  CURRENT FILING DATE:  2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/090,411
;  PRIOR FILING DATE: 1998-06-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:anti-sense
;   OTHER INFORMATION: primer
US-10-326-681-24

  Query Match             82.1%;  Score 32;  DB 15;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              ||||||||||||||||||||||||||||||||
Db         32 CCCAGTTTTCTGTTTTATTACCAAGACATTAA 1


RESULT 9
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29328
;   LENGTH: 678
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-29328

  Query Match             61.5%;  Score 24;  DB 13;  Length 678;
  Best Local Similarity   84.4%;  Pred. No. 38;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
              |||||||||||||||||||| |   ||| |
Db        324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 10
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329

Query Match 61.5%; Score 24; DB 13; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
||||||||||||||||||||||| | |||
Db 324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293

RESULT 11
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29328
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29328

Query Match 61.5%; Score 24; DB 15; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
||||||||||||||||||||||| | |||
Db 324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293

RESULT 12
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329

Query Match 61.5%; Score 24; DB 15; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
||||||||||||||||||||||| | |||
Db 324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293

RESULT 13
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31882
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-31882

Query Match 61.5%; Score 24; DB 13; Length 808;
Best Local Similarity 84.4%; Pred. No. 40;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
              ||||||||||||||||||||| |   ||| |
Db        324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 14
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31882
;   LENGTH: 808
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-31882

  Query Match             61.5%;  Score 24;  DB 15;  Length 808;
  Best Local Similarity   84.4%;  Pred. No. 40;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TATGGCCCAGTTTTCTGTTTTATTACCAAGAC 34
              ||||||||||||||||||||| |   ||| |
Db        324 TATGGCCCAGTTTTCTGTTTTACTGAGAAGGC 293


RESULT 15
US-10-076-747-54/c
; Sequence 54, Application US/10076747
; Publication No. US20030180726A1
; GENERAL INFORMATION:
;  APPLICANT: Salceda, Susana
;  APPLICANT:  Macina, Roberto
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Karra, Kalpana
;  APPLICANT:  Cafferkey, Robert
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P
;  FILE REFERENCE: DEX-0315
;  CURRENT APPLICATION NUMBER: US/10/076,747
;  CURRENT FILING DATE:  2002-02-13
;  PRIOR APPLICATION NUMBER: 60/268,290
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 60/268,834
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 554
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-076-747-54

  Query Match             59.0%;  Score 23;  DB 15;  Length 554;
  Best Local Similarity   83.9%;  Pred. No. 87;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TATGGCCCAGTTTTCTGTTTTATTACCAAGA 33
              | || |||||||||| |||| | ||||||||
Db        201 TTTGTCCCAGTTTTCCGTTTCAATACCAAGA 171


Search completed: February  1, 2005, 17:20:32
Job time : 54.6349 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 438.493 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
Sequence: 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	39	100.0	257	1	AI919501	AI919501 tp22b01.x
	2	39	100.0	358	2	BE768971	PM4-FT002
c	3	39	100.0	401	1	AI674711	wd19e10.x
c	4	39	100.0	491	1	AA635142	af10e10.s
c	5	39	100.0	568	7	CO586973	DG2-13911
c	6	39	100.0	570	6	CD364939	UI-H-FT2-
c	7	39	100.0	600	7	CO701132	DG32-195b
	8	39	100.0	612	7	CN409515	170006001
	9	39	100.0	638	7	CN409513	170005327
	10	39	100.0	681	4	BM784030	K-EST0062
c	11	39	100.0	684	6	CD364946	UI-H-FT2-
	12	39	100.0	819	2	BF981023	602310222
	13	39	100.0	836	1	AL048242	DKFZp586O
	14	39	100.0	836	4	BG574734	602596770
	15	39	100.0	900	5	BX390237	BX390237
c	16	39	100.0	903	5	BX371508	BX371508
c	17	39	100.0	911	5	BX350035	BX350035
	18	39	100.0	950	7	CF413058	CH3#083_G
	19	39	100.0	975	4	BM472910	AGENCOURT
	20	39	100.0	1064	5	BX459089	BX459089
	21	39	100.0	1380	3	BC012316	Homo sapi
	22	38.6	99.0	1075	1	AL543068	AL543068
	23	37	94.9	659	4	BG572739	602594259
c	24	36	92.3	330	5	BX102948	BX102948 BX102948
	25	35.8	91.8	388	1	AJ686857	AJ686857 AJ686857
	26	35.8	91.8	421	1	AJ667166	AJ667166 AJ667166
c	27	35.8	91.8	429	1	AV667881	AV667881 AV667881
	28	35.8	91.8	477	4	BG938257	BG938257 1Abo14E09
	29	35.8	91.8	484	7	CF930825	CF930825 CF--05-R-
	30	35.8	91.8	562	4	BI774611	BI774611 466793 MA
c	31	35.8	91.8	581	6	CB538214	CB538214 776179 MA
	32	35.8	91.8	586	7	CN441464	CN441464 BE04026A1
	33	35.8	91.8	648	5	BQ599498	BQ599498 MI-P-E6-a
	34	35.8	91.8	682	7	CN788377	CN788377 4122709 B
c	35	34	87.2	127	1	AA503765	AA503765 ne50h09.s
	36	33.2	85.1	609	6	CD535426	CD535426 LeukoN5_4
c	37	33	84.6	205	2	BF431095	BF431095 7o07b11.x
	38	32.6	83.6	303	6	CA535795	CA535795 C0224B10-
	39	32.6	83.6	351	6	CF269885	CF269885 OKST Rat
	40	32.6	83.6	429	4	BG797326	BG797326 ic13h12.x
	41	32.6	83.6	443	6	CA536077	CA536077 C0228H03-
	42	32.6	83.6	529	6	CB545374	CB545374 AMGNNUC:C
	43	32.6	83.6	541	6	CA533816	CA533816 C0406H10-
	44	32.6	83.6	546	7	CK333529	CK333529 H8247H08-
	45	32.6	83.6	557	7	CK364324	CK364324 AGENCOURT

ALIGNMENTS

RESULT 1
AI919501/c
LOCUS AI919501 257 bp mRNA linear EST 14-DEC-1999
DEFINITION tp22b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188489 3' similar to SW:MTAP_HUMAN Q13126 5'-METHYLTHIOADENOSINE PHOSPHORYLASE ;, mRNA sequence.
ACCESSION AI919501
VERSION AI919501.1 GI:5639356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 257)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 246.
FEATURES Location/Qualifiers
source 1. .257
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2188489"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
ORIGIN

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  Query Match            100.0%;  Score 39;  DB 1;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 0.0015;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
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RESULT 2
BE768971
LOCUS       BE768971                358 bp    mRNA    linear   EST 20-SEP-2000
DEFINITION  PM4-FT0023-020600-001-d09 FT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE768971
VERSION     BE768971.1  GI:10222629
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM4-FT0023-020
            600-001-d09&t3=2000-06-02&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 18
            High quality sequence stop: 358.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="FT0023"
                     /note="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match            100.0%;  Score 39;  DB 2;  Length 358;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db         48 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 86


RESULT 3
AI674711/c
LOCUS       AI674711                401 bp    mRNA    linear   EST 19-MAY-1999
DEFINITION  wd19e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2328618 3' similar to SW:MTAP_HUMAN Q13126
            5'-METHYLTHIOADENOSINE PHOSPHORYLASE ;, mRNA sequence.
ACCESSION   AI674711
VERSION     AI674711.1  GI:4875191
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .401
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2328618"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match            100.0%;  Score 39;  DB 1;  Length 401;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        247 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 209


RESULT 4
AA635142/c
LOCUS       AA635142                491 bp    mRNA    linear   EST 21-OCT-1997
DEFINITION  af10e10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031274
            3' similar to TR:G847724 G847724 METHYLTHIOADENOSINE PHOSPHORYLASE.
            ;, mRNA sequence.
ACCESSION   AA635142
VERSION     AA635142.1  GI:2558356
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
```

```
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 289.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1031274"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares_testis_NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match             100.0%;  Score 39;  DB 1;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        371 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 333


RESULT 5
CO586973/c
LOCUS       CO586973                568 bp    mRNA    linear   EST 21-JUL-2004
DEFINITION  DG2-139111 DG2-brain Canis familiaris cDNA 3', mRNA sequence.
ACCESSION   CO586973
VERSION     CO586973.1  GI:50432494
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 568)
  AUTHORS   Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
            Henrich,J. and Loebbert,R.
  TITLE     Dog arrayTAG cDNA clone collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas Schlueter
            LION bioscience AG
            Waldhoferstrasse 98, D-69123 Heidelberg, Germany
            Tel: +49 6221 4038 150
            Fax: +49 6221 4038 290
            Email: Thomas.Schlueter@lionbioscience.com.
FEATURES             Location/Qualifiers
     source          1. .568
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /strain="Beagle"
                     /db_xref="taxon:9615"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="DG2-brain"
                     /note="Organ: brain; Vector: Dog pBluescript LION"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 7;  Length 568;
  Best Local Similarity   100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        379 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 341


RESULT 6
CD364939/c
LOCUS       CD364939                570 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT2-bjn-i-17-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.
ACCESSION   CD364939
VERSION     CD364939.1  GI:31149029
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjn-i-17-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella  moi 10, 24 hours; Staph
                     aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
                     adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
                     hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
                     wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
                     The library was subtracted according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. The tissue
                     was provided by Dr. Gary W. Hunninghake of the University
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of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
ORIGIN

Query Match 100.0%; Score 39; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
||||||||||||||||||||||||||||||||||||||||
Db 404 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 366

RESULT 7
CO701132/c
LOCUS CO701132 600 bp mRNA linear EST 26-JUL-2004
DEFINITION DG32-195b11 DG32-liver Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO701132
VERSION CO701132.1 GI:50649800
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 600)
AUTHORS Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
Henrich,J. and Loebbert,R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
FEATURES Location/Qualifiers
source 1. .600
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: Dog pBluescript LION"
ORIGIN

Query Match 100.0%; Score 39; DB 7; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
||||||||||||||||||||||||||||||||||||||||
Db 359 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 321

RESULT 8
CN409515
LOCUS CN409515 612 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600188932 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409515
VERSION CN409515.1 GI:47396639
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 612)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 612 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .612
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
ORIGIN

Query Match 100.0%; Score 39; DB 7; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
||||||||||||||||||||||||||||||||||||||||
Db 230 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 268

RESULT 9
CN409513
LOCUS CN409513 638 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409513
VERSION CN409513.1 GI:47396637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 638)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 638 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN

```
  Query Match           100.0%;  Score 39;  DB 7;  Length 638;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        591 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 629


RESULT 10
BM784030
LOCUS       BM784030                681 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0062086 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-F01 5',
            mRNA sequence.
ACCESSION   BM784030
VERSION     BM784030.1  GI:19132262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 32  row: F  column: 01
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S6SNU620-32-F01"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Scattering floating"
                     /cell_line="SNU-620"
                     /lab_host="Top10F'"
                     /clone_lib="S6SNU620"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match           100.0%;  Score 39;  DB 4;  Length 681;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        312 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 350


RESULT 11
CD364946/c
LOCUS       CD364946                684 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT2-bjn-k-07-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjn-k-07-0-UI 3', mRNA sequence.
ACCESSION   CD364946
VERSION     CD364946.1  GI:31149036
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjn-k-07-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella  moi 10, 24 hours; Staph
                     aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
                     adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
                     hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
                     wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
                     The library was subtracted according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. The tissue
                     was provided by Dr. Gary W. Hunninghake of the University
                     of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT2
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match           100.0%;  Score 39;  DB 6;  Length 684;
  Best Local Similarity  100.0%;  Pred. No. 0.0016;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        404 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 366


RESULT 12
BF981023
LOCUS       BF981023                819 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  602310222F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4401533 5',
            mRNA sequence.
ACCESSION   BF981023
VERSION     BF981023.1  GI:12383835
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10108  row: k  column: 06
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4401533"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 39;  DB 2;  Length 819;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        115 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 153


RESULT 13
AL048242
LOCUS       AL048242                836 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp586O1023_r1 586 (synonym: hute1) Homo sapiens cDNA clone
            DKFZp586O1023, mRNA sequence.
ACCESSION   AL048242
VERSION     AL048242.1  GI:4729075
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Ansorge, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp586O1023) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp586O1023"
                     /tissue_type="uterus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="586 (synonym: hute1)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
ORIGIN

  Query Match             100.0%;  Score 39;  DB 1;  Length 836;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db        321 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 359


RESULT 14
BG574734
LOCUS       BG574734                836 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602596770F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705673 5',
            mRNA sequence.
ACCESSION   BG574734
VERSION     BG574734.1  GI:13582387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10572  row: k  column: 18
            High quality sequence stop: 680.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4705673"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_87"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
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                    Average insert size 1.383 kb. Library enriched for
                    full-length clones and constructed by Life Technologies.
                    Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 39;  DB 4;  Length 836;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db         22 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 60


RESULT 15
BX390237
LOCUS       BX390237                900 bp    mRNA    linear   EST 28-APR-2004
DEFINITION  BX390237 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YH04 5-PRIME, mRNA sequence.
ACCESSION   BX390237
VERSION     BX390237.2  GI:46834877
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30461423.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAG024ZA09_CS02273_1&c=5445.f

FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI002YH04"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             100.0%;  Score 39;  DB 5;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 39
              |||||||||||||||||||||||||||||||||||||||
Db         58 AATATGGCCCAGTTTTCTGTTTTATTACCAAGACATTAA 96


Search completed: February  1, 2005, 14:58:29
Job time : 439.493 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 691.095 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGGACCGGGTCTT.....AAACCCTCCATAACCTGAAG 123

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	123	100.0	303	9	AH013410S7	L42633 Homo sapien
2	123	100.0	499	6	AR425810	AR425810 Sequence
3	123	100.0	499	6	AX986504	AX986504 Sequence
4	123	100.0	499	6	BD121363	BD121363 EST and e
5	123	100.0	849	9	CR541710	CR541710 Homo sapi
6	123	100.0	852	9	CR541670	CR541670 Homo sapi
7	123	100.0	870	6	AX826996	AX826996 Sequence
8	123	100.0	1021	9	L40432	L40432 Homo sapien
9	123	100.0	1890	9	BC026106	BC026106 Homo sapi
10	123	100.0	2269	9	HSU22233	U22233 Human methy
11	123	100.0	2763	6	AR059583	AR059583 Sequence
12	123	100.0	2763	6	I28320	I28320 Sequence 1
13	123	100.0	2763	6	AR473576	AR473576 Sequence
14	123	100.0	2763	6	AR474046	AR474046 Sequence
15	123	100.0	3083	6	AR144466	AR144466 Sequence
16	123	100.0	3083	6	AR342446	AR342446 Sequence
17	123	100.0	168656	9	AL359922	AL359922 Human DNA
18	123	100.0	250000	9	AB060808	AB060808 Homo sapi
19	100.6	81.8	807	9	L42635	L42635 Homo sapien
c 20	100.6	81.8	94125	9	AC016966	AC016966 Homo sapi
c 21	100.6	81.8	168366	2	AC069409	AC069409 Homo sapi
c 22	100.6	81.8	180606	2	AC073406	AC073406 Homo sapi
23	95.8	77.9	1055	10	AB056100	AB056100 Mus muscu
24	95.8	77.9	2565	10	BC003858	BC003858 Mus muscu
c 25	95.8	77.9	194025	10	AL831719	AL831719 Mouse DNA
c 26	94.2	76.6	225782	2	AC109529	AC109529 Rattus no
c 27	94.2	76.6	287775	2	AC108638	AC108638 Rattus no
c 28	88.2	71.7	170899	2	AC144208	AC144208 Macaca mu
29	60.4	49.1	230762	2	AC097556	AC097556 Rattus no
c 30	60.4	49.1	232771	2	AC128406	AC128406 Rattus no
31	55	44.7	151290	10	AC121902	AC121902 Mus muscu
32	52.4	42.6	90801	9	AC025033	AC025033 Homo sapi
c 33	52.4	42.6	146349	2	AC012027	AC012027 Homo sapi
c 34	52.4	42.6	171615	2	AC089988	AC089988 Homo sapi
35	52.4	42.6	212382	2	AC010936	AC010936 Homo sapi
c 36	50	40.7	8319	5	FRU250231	AJ250231 Fugu rubr
37	46.2	37.6	1255	5	BC056545	BC056545 Danio rer
38	46.2	37.6	1265	5	BC046035	BC046035 Danio rer
c 39	46.2	37.6	150073	5	BX323448	BX323448 Zebrafish
40	46.2	37.6	161859	2	CR385087	CR385087 Danio rer
41	46.2	37.6	245135	2	AC095099	AC095099 Rattus no
c 42	34.2	27.8	236746	2	AC119312	AC119312 Rattus no
c 43	34	27.6	174697	9	AP002370	AP002370 Homo sapi
c 44	34	27.6	184516	2	AC018708	AC018708 Homo sapi
c 45	34	27.6	197847	9	AP002751	AP002751 Homo sapi

ALIGNMENTS

RESULT 1
AH013410S7
LOCUS AH013410S7 - 303 bp DNA linear PRI 01-DEC-2003
DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 7.
ACCESSION L42633
VERSION L42633.1 GI:38570313
KEYWORDS .
SEGMENT 7 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 303)
AUTHORS Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.
TITLE Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
MEDLINE 96234115
PUBMED 8650244
FEATURES Location/Qualifiers
source 1. .303
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22-p21"
/clone="cMII5"
/tissue_type="placenta"
exon 76. .198
/gene="MTAP"
/note="putative"
/number=7
ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db         76 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 135
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Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 195

Qy        121 AAG 123
              |||
Db        196 AAG 198


RESULT 2
AR425810
LOCUS       AR425810                 499 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17307 from patent US 6639063.
ACCESSION   AR425810
VERSION     AR425810.1  GI:40180920
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 17307 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 295

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 355

Qy        121 AAG 123
              |||
Db        356 AAG 358


RESULT 3
AX986504
LOCUS       AX986504                 499 bp    DNA     linear   PAT 15-JAN-2004
DEFINITION  Sequence 17307 from Patent EP1104808.
ACCESSION   AX986504
VERSION     AX986504.1  GI:40992644
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
  TITLE     ESTs and encoded human proteins
  JOURNAL   Patent: EP 1104808-A 17307 06-JUN-2001;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.6e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 355

Qy        121 AAG 123
              |||
Db        356 AAG 358


RESULT 4
BD121363
LOCUS       BD121363                 499 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  EST and encoded human protein.
ACCESSION   BD121363
VERSION     BD121363.1  GI:23216273
KEYWORDS    JP 2002010789-A/13440.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
  TITLE     EST and encoded human protein
  JOURNAL   Patent: JP 2002010789-A 13440 15-JAN-2002;
            GENSET CORP        .
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002010789-A/13440
            PD   15-JAN-2002
            PF   07-AUG-2000 JP 2000280989
            PR   05-AUG-1999 US    60/147499
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE  PI
             GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
            C12N15/00
            CC   EST and encoded human protein
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        236 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 295

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 355

Qy        121 AAG 123
              |||
Db        356 AAG 358


RESULT 5
CR541710
LOCUS       CR541710                 849 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834H1128D for
```

gene MTAP, methylthioadenosine phosphorylase; complete cds, without stopcodon.
ACCESSION CR541710
VERSION CR541710.1 GI:49456380
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 849)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 849)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPDo834H1128D, ORFNo 3404
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834H1128D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH131058.01L
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found AA exchange(s) at position (first base of changed triplet): 133(leu->ser) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES Location/Qualifiers
source 1. .849
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDo834H1128D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
gene 1. .849
/gene="MTAP"
CDS 1. .>849
/gene="MTAP"
/codon_start=1
/protein_id="CAG46511.1"
/db_xref="GI:49456381"
/translation="MASGTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
SILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
SVLLPRH"
ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 691 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 750

Qy 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 810

Qy 121 AAG 123
|||
Db 811 AAG 813

RESULT 6
CR541670
LOCUS CR541670 852 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPDo834G1127D for gene MTAP, methylthioadenosine phosphorylase; complete cds, incl. stopcodon.
ACCESSION CR541670
VERSION CR541670.1 GI:49456300
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 852)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 852)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPDo834G1127D, ORFNo 3305
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834G1127D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found

```
           AA exchange(s) at position (first base of changed triplet):
           139(leu->met) 166(ile->val)
           Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES             Location/Qualifiers
     source          1. .852
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RZPDo834G1127D"
                     /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                     /lab_host="DH5Alpha"
                     /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene            1. .852
                     /gene="MTAP"
     CDS             1. .852
                     /gene="MTAP"
                     /codon_start=1
                     /protein_id="CAG46471.1"
                     /db_xref="GI:49456301"
                     /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LIMGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 123;  DB 9;  Length 852;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 750

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 810

Qy        121 AAG 123
              |||
Db        811 AAG 813


RESULT 7
AX826996
LOCUS       AX826996                 870 bp    DNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 1 from Patent WO03074083.
ACCESSION   AX826996
VERSION     AX826996.1  GI:39837205
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bloom,L.A., Boritzki,T.J., Kung,P.P., Ogden,R.C., Skalitzky,D.J.,
            Zehnder,L.R., Kuhn,L.A. and Meng,J.J.
  TITLE     Combination therapies for treating methylthioadenosine
            phosphorylase deficient cells
  JOURNAL   Patent: WO 03074083-A 1 12-SEP-2003;
            PFIZER INC. (US)
FEATURES             Location/Qualifiers
     source          1. .870
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Cloned MTAP cDNA"
ORIGIN

  Query Match           100.0%;  Score 123;  DB 6;  Length 870;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 756

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 816

Qy        121 AAG 123
              |||
Db        817 AAG 819


RESULT 8
L40432
LOCUS       L40432                   1021 bp    mRNA    linear   PRI 12-DEC-2000
DEFINITION  Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
            complete cds.
ACCESSION   L40432
VERSION     L40432.1  GI:11602391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Genomic cloning of methylthioadenosine phosphorylase: a purine
            metabolic enzyme deficient in multiple different cancers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
  MEDLINE   96234115
   PUBMED   8650244
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
            Research on Aging, and Department of Medicine, University of
            California at San Diego, La Jolla, CA 92093-0663, USA
COMMENT     GSDB:S:39613.
            [Flatfile retrieved from GSDB Thu Dec  7 15:18:48 2000].
FEATURES             Location/Qualifiers
     source          1. .1021
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p22-p21"
                     /tissue_type="placenta"
                     /tissue_lib="lambda gt11"
     gene            1. .1021
                     /gene="MTAP"
     CDS             111. .962
                     /gene="MTAP"
                     /EC_number="2.4.2.28"
                     /note="putative"
                     /codon_start=1
                     /product="methylthioadenosine phosphorylase"
                     /protein_id="AAG38871.1"
                     /db_xref="GI:11602392"
                     /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 123;  DB 9;  Length 1021;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 860

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 920

Qy        121 AAG 123
              |||
Db        921 AAG 923
```

RESULT 9
BC026106
LOCUS BC026106 1890 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone MGC:33067 IMAGE:4820938), complete cds.
ACCESSION BC026106
VERSION BC026106.1 GI:19913486
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1890)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1890)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 46 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6006025.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:33067 IMAGE:4820938"
                     /tissue_type="Brain, hippocampus"
                     /clone_lib="NIH_MGC_95"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
     gene            1. .1890
                     /gene="MTAP"
                     /note="synonyms: MSAP, c86fus"
                     /db_xref="LocusID:4507"
                     /db_xref="MIM:156540"
     CDS             96. .947
                     /gene="MTAP"
                     /codon_start=1
                     /product="5'-methylthioadenosine phosphorylase"
                     /protein_id="AAH26106.1"
                     /db_xref="GI:19913487"
                     /db_xref="LocusID:4507"
                     /db_xref="MIM:156540"
                     /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
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                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN
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Query Match 100.0%; Score 123; DB 9; Length 1890;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        786 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 845

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 905

Qy        121 AAG 123
              |||
Db        906 AAG 908
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RESULT 10
HSU22233
LOCUS HSU22233 2269 bp mRNA linear PRI 25-NOV-1995
DEFINITION Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.
ACCESSION U22233
VERSION U22233.1 GI:847723
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2269)
AUTHORS Olopade,O.I., Pomykala,H.M., Hagos,F., Sveen,L.W., Espinosa,R. III, Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and Bohlander,S.K.
TITLE Construction of a 2.8-megabase yeast artificial chromosome contig and cloning of the human methylthioadenosine phosphorylase gene from the tumor suppressor region on 9p21
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
MEDLINE 95327672
PUBMED 7604019
REFERENCE 2 (bases 1 to 2269)
AUTHORS Olopade,O.I.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,

```
            University of Chicago Pritzker School of Medicine, 5841 S. Maryland
            Avenue, Chicago, IL 60637-1470, USA
FEATURES              Location/Qualifiers
     source           1. .2269
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                      /chromosome="9"
                      /map="9p21"
                      /clone="18-11 cDNA"
                      /sex="male"
                      /cell_line="primary culture"
                      /cell_type="fibroblast"
                      /tissue_type="epidermis"
     gene             1. .2269
                      /gene="MTAP"
     CDS              122. .973
                      /gene="MTAP"
                      /codon_start=1
                      /product="methylthioadenosine phosphorylase"
                      /protein_id="AAA81646.1"
                      /db_xref="GI:847724"
                      /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                      LILGKIKNVDCILLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
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                      LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                      TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                      SVLLPRH"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 9;  Length 2269;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 871

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 931

Qy        121 AAG 123
              |||
Db        932 AAG 934


RESULT 11
AR059583
LOCUS       AR059583                2763 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5840505.
ACCESSION   AR059583
VERSION     AR059583.1  GI:5986033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
  TITLE     Method for inhibiting adenylosuccinate synthetase activity in
            methylthioadenosine phosphorylase deficient cells
  JOURNAL   Patent: US 5840505-A 1 24-NOV-1998;
FEATURES              Location/Qualifiers
     source           1. .2763
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 12
I28320
LOCUS       I28320                  2763 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571510.
ACCESSION   I28320
VERSION     I28320.1  GI:1819096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Nobori,T. and Carson,D.A.
  TITLE     Method for selective methionine starvation of malignant cells in
            mammals
  JOURNAL   Patent: US 5571510-A 1 05-NOV-1996;
FEATURES              Location/Qualifiers
     source           1. .2763
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 13
AR473576
LOCUS       AR473576                2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689561.
ACCESSION   AR473576
VERSION     AR473576.1  GI:42711901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Tumor suppressor gene and methods for detection of cancer,
            monitoring of tumor progression and cancer treatment
  JOURNAL   Patent: US 6689561-A 14 10-FEB-2004;
FEATURES              Location/Qualifiers
     source           1. .2763
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-28;
```

```
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 14
AR474046
LOCUS       AR474046               2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689864.
ACCESSION   AR474046
VERSION     AR474046.1  GI:42712799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Cyclin dependent kinase 4 inhibitor
  JOURNAL   Patent: US 6689864-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 123;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 15
AR144466
LOCUS       AR144466               3083 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6210917.
ACCESSION   AR144466
VERSION     AR144466.1  GI:15106333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A. and Carrera,C.J.
  TITLE     Method for suppressing multiple drug resistance in cancer cells
  JOURNAL   Patent: US 6210917-A 1 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .3083
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 123;  DB 6;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-28;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||
Db       2546 AAG 2548


Search completed: February  1, 2005, 13:26:00
Job time : 693.095 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 161.422 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGGACCGGGTCTT.....AAACCCTCCATAACCTGAAG 123

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	123	100.0	870	10	ADC37133	Adc37133 Cloned me
2	123	100.0	2197	10	ADC30327	Adc30327 Human nov
3	123	100.0	2763	2	AAT15167	Aat15167 Methylthi
4	123	100.0	2763	2	AAQ92813	Aaq92813 Human MTA
5	123	100.0	2763	2	AAT85305	Aat85305 Human met
6	123	100.0	2763	2	AAZ00866	Aaz00866 Human MTA
7	123	100.0	2763	5	AAF86091	Aaf86091 Methylthi
8	123	100.0	2763	10	AAD64097	Aad64097 Human met
9	123	100.0	2784	2	AAQ99202	Aaq99202 Pseudomon
10	123	100.0	3083	2	AAX58284	Aax58284 Human met
11	123	100.0	3083	8	ABX10818	Abx10818 DNA encod
12	113	91.9	1437	4	AAH33683	Aah33683 Human col
13	41.2	33.5	662	6	ABQ59125	Abq59125 Human col
c 14	31.2	25.4	603	6	ABQ59540	Abq59540 Human col
c 15	31	25.2	145831	6	ABL69213	Abl69213 Prostate
c 16	31	25.2	145831	6	ABL66806	Abl66806 Lung canc
c 17	31	25.2	145831	6	ABL68588	Abl68588 Kidney ca
c 18	31	25.2	145831	6	ABL62309	Abl62309 Colon ade
c 19	31	25.2	145831	6	ABT10149	Abt10149 Human bre
c 20	29.8	24.2	760	6	ABQ16984	Abq16984 Oligonucl
21	29.8	24.2	760	6	ABQ16985	Abq16985 Oligonucl
c 22	29.8	24.2	61557	4	AAS59521	Aas59521 Propionib
c 23	29.8	24.2	61557	8	ACF64450	Acf64450 Propionib
c 24	29.2	23.7	2207	10	ADD89080	Add89080 Encoding
c 25	29.2	23.7	2207	12	ADL91576	Adl91576 Human imm
c 26	29.2	23.7	2213	8	ABZ35866	Abz35866 Human sec
c 27	29.2	23.7	3103	8	ABZ36155	Abz36155 Human sec
c 28	29.2	23.7	6815	11	ADL22655	Adl22655 Human dis
c 29	29	23.6	7746	6	ABK40047	Abk40047 Human che
c 30	29	23.6	7746	6	ABL33856	Abl33856 Human imm
c 31	28.8	23.4	2891	10	ADH54930	Adh54930 Human ins
c 32	28.4	23.1	14112	4	AAS46477	Aas46477 Tumour su
c 33	28.4	23.1	14112	6	ABL33442	Abl33442 Human imm
c 34	28.4	23.1	14112	6	ABK31332	Abk31332 Signal tr
c 35	28.4	23.1	14112	6	ABQ66979	Abq66979 Human ang
c 36	28.2	22.9	6098	6	ABL32519	Abl32519 Human imm
c 37	28.2	22.9	9258	4	ABL12730	Abl12730 Drosophil
c 38	28.2	22.9	17077	10	ADD48825	Add48825 Human gen
c 39	28.2	22.9	24419	4	ABL10682	Abl10682 Drosophil
c 40	28.2	22.9	24419	4	ABL18670	Abl18670 Drosophil
c 41	28.2	22.9	61020	4	AAS46788	Aas46788 Tumour su
42	28	22.8	223	9	ADA09632	Ada09632 Restricti
c 43	28	22.8	419	5	ABV10652	Abv10652 Human pro
44	28	22.8	1794	3	AAA30256	Aaa30256 Rat parti
45	28	22.8	2286	12	ADI81563	Adi81563 Rat stret

ALIGNMENTS

RESULT 1
ADC37133
ID ADC37133 standard; cDNA; 870 BP.
XX
AC ADC37133;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cloned methylthioadenosine phosphorylase, MTAP, cDNA.
XX
KW combination therapy; methylthioadenosine phosphorylase; MTAP; inhibitor;
KW glycinamide ribonucleotide formyltransferase; GARFT;
KW aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX
OS Unidentified.
XX
PN WO2003074083-A1.
XX
PD 12-SEP-2003.
XX
PF 17-FEB-2003; 2003WO-IB000615.
XX
PR 04-MAR-2002; 2002US-0361645P.
PR 09-DEC-2002; 2002US-0432275P.
XX
PA (PFIZ) PFIZER INC.
XX
PI Bloom LA, Boritzki TJ, Kung P, Ogden RC, Skalitzky DJ;
PI Zehnder LR, Kuhn LA, Meng JJ;
XX
DR WPI; 2003-748252/70.
XX
PT Selectively killing methylthioadenosine phosphorylase deficient cells
PT used for treating cell proliferative disorders comprises administering
PT glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX
PS Example 3B; Page 182-183; 189pp; English.
XX
CC This invention relates to novel combination therapies that selectively
CC kill methylthioadenosine phosphorylase (MTAP) deficient cells. The
CC combination therapies comprise administering an inhibitor of glycinamide

```
CC   ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC   ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC   toxicity agent during and after administration of the inhibitor. The
CC   combination therapies can be used for selectively killing MTAP deficient
CC   cells, and for treating cell proliferative disorders e.g. lung cancer,
CC   leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC   prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC   The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC   MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC   dose of the inhibitor. This polynucleotide sequence represents the cloned
CC   MTAP cDNA of the invention.
XX
SQ   Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 123;  DB 10;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 756

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 816

Qy        121 AAG 123
              |||
Db        817 AAG 819


RESULT 2
ADC30327
ID   ADC30327 standard; cDNA; 2197 BP.
XX
AC   ADC30327;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human novel cDNA sequence, SEQ ID NO:409.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; chromosome 3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003029271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY,  Zhang J,  Ren F,  Xue AJ,  Zhao QA,  Wang J,  Wehrman T;
PI   Zhou P,  Ghosh M,  Wang D,  Ma Y,  Asundi V,  Wang Z,  Weng G;
PI   Haley-Vicente D,  Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC31298.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet
PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 409; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
CC   recombinant production of a polypeptide of the invention; an antibody
CC   against a polypeptide of the invention; a method of detecting
CC   polynucleotides or polypeptides of the invention; and methods of
CC   identifying a compound which binds to a polypeptide of the invention. The
CC   invention further discloses methods of peventing, treating or
CC   ameliorating a medical condition; kits comprising polynucleotide probes
CC   and/or monoclonal antibodies for carrying out the methods of the
CC   invention; methods for the identification of compounds that modulate the
CC   expression or activity of the polynucleotide and/or polypeptide; and 767
CC   contig sequences corresponding to the cDNA sequences of the invention
CC   (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC   -ADC33394). The nucleic acids and polypeptides of the invention are
CC   useful in diagnostics, drug screening, forensics, gene mapping, in the
CC   identification of mutations responsible for genetic disorders or other
CC   traits, for assessing biodiversity, and in producing many other types of
CC   data and products dependent on DNA and amino acid sequences. They are
CC   also used for treating diseases such as Parkinson's disease, Alzheimer's
CC   disease and other neurodegenerative diseases, anaemia, platelet
CC   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC   cancer. The nucleic acids may also be used as hybridisation probes or
CC   primers, and in the recombinant production of a protein. The polypeptides
CC   are also useful in generating antibodies, as molecular weight markers,
CC   and as food supplements. The present sequence represents a specifically
CC   claimed human cDNA sequence of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 123;  DB 10;  Length 2197;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 810

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 870

Qy        121 AAG 123
              |||
Db        871 AAG 873


RESULT 3
AAT15167
ID   AAT15167 standard; DNA; 2763 BP.
XX
AC   AAT15167;
XX
DT   29-JUN-1996  (first entry)
XX
DE   Methylthioadenosine-phosphorylase gene.
XX
KW   Human; methylthioadenosine-phosphorylase; chromosome walking;
KW   interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW   cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW   melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW   non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW   antibody; imaging; ss.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= b
FT   intron          422. .615
FT                   /*tag= c
FT   exon            616. .720
FT                   /*tag= d
FT   intron          721. .963
FT                   /*tag= e
FT   exon            964. .1203
FT                   /*tag= f
XX
PN   WO9528169-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;   95WO-US004655.
XX
PR   14-APR-1994;   94US-00227800.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 1995-373630/48.
XX
PT   Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT   useful for diagnosis, assessing predisposition and treatment of cancers.
XX
PS   Example 1; Page 96-101; 129pp; English.
XX
CC   The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC   at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC   tumour suppressor gene (AAT15157-58) is located between this gene and an
CC   interferon-alpha gene cluster, and has been isolated by chromosome
CC   walking. The CDK4I gene, probe and primer derivatives and the gene
CC   product may be used in diagnosis of cancer, particularly melanoma
CC   (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC   carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC   or in antitumour antisense oligonucleotide or ribozyme construction.
CC   Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 4
AAQ92813
ID   AAQ92813 standard; DNA; 2763 BP.
XX
AC   AAQ92813;
XX
DT   25-MAR-2003  (revised)
DT   05-DEC-1995  (first entry)
XX
DE   Human MTAse.
XX
KW   MTAse; methyladenosine-phosphatase; malignancy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= a
FT   exon            616. .720
FT                   /*tag= b
FT   exon            964. .1203
FT                   /*tag= c
FT   exon            1640. .1762
FT                   /*tag= d
FT   exon            2272. .2310
FT                   /*tag= e
XX
PN   WO9518233-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014920.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CIBA ) CIBA GEIGY CORP.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 1995-246398/32.
XX
PT   Detecting methyl:adenosine phosphatase in mammalian cells - by
PT   hybridisation with specific oligonucleotide for detecting malignancy,
PT   also new nucleic acid, expression vectors, derived polypeptide(s) and
PT   antibodies.
XX
PS   Claim 8; Page 34-35; 47pp; English.
XX
CC   A cosmid gene library constructed from human placenta DNA was screened
CC   using a MTAse cDNA probe to isolate a human MTAse genomic clone (sequence
CC   given in AAQ92813). Absence of MTAse from a cell is indicative of
CC   malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 5
AAT85305
ID   AAT85305 standard; DNA; 2763 BP.
XX
AC   AAT85305;
XX
DT   28-FEB-1998  (first entry)
XX
DE   Human methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
```

```
KW   adenylsuccinate synthetase; lung cancer; glioma;
KW   acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= a
FT                   /number= 1
FT   intron          422. .615
FT                   /*tag= b
FT                   /number= 1
FT   exon            616. .720
FT                   /*tag= c
FT                   /number= 2
FT   intron          721. .963
FT                   /*tag= d
FT                   /number= 2
FT   exon            964. .1203
FT                   /*tag= e
FT                   /number= 3
XX
PN   WO9732994-A1.
XX
PD   12-SEP-1997.
XX
PF   27-JAN-1997;   97WO-US001193.
XX
PR   08-MAR-1996;   96US-00612542.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 1997-470550/43.
XX
PT   Inhibiting adenyl:succinate synthetase activity in methylthio:adenosine
PT   phosphorylase-deficient cells - by treatment with specific inhibitor,
PT   especially L-alanosine, useful for selective killing of MTAse deficient
PT   cancer cells.
XX
PS   Example 3; Page 25-26; 37pp; English.
XX
CC   This DNA sequence comprises human genomic DNA for methylthioadenosine
CC   phosphorylase (MTase), obtained from a cosmid gene library constructed
CC   from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC   method for inhibiting the activity adenylsuccinate synthetase (ASS) in
CC   mammalian cells deficient in MTAse activity involves: (a) determining
CC   that a population of cells obtained from a mammalian host is MTase
CC   deficient; and (b) administering an ASS inhibitor (preferably L-
CC   alanosine) to the host so that the MTase deficient host cells are
CC   depleted of AMP. The method is especially used to treat human MTAse-
CC   deficient primary tumour cells, specifically non-small cell lung cancer,
CC   acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC   MTAse catabolises methylthioadenosine to adenine for endogenous salvage
CC   incorporation into the intracellular AMP pool. The claimed method
CC   deprives the cells of substrate for de novo synthesis of AMP, resulting
CC   in selective killing of these cells. MTAse sequence-specific
CC   oligonuclotides can be used to detect the presence or absence of MTAse in
CC   malignant cell lines
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

  Query Match            100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
               |||
Db       1760 AAG 1762


RESULT 6
AAZ00866
ID   AAZ00866 standard; DNA; 2763 BP.
XX
AC   AAZ00866;
XX
DT   20-OCT-1999  (first entry)
XX
DE   Human MTAse DNA.
XX
KW   MTAse; methylthioadenosine phosphorylase; human; detection; active;
KW   catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            253. .421
FT                   /*tag= a
FT                   /number= 1
FT                   /note= "Putative exon"
FT   intron          422. .615
FT                   /*tag= b
FT                   /number= 1
FT                   /note= "putative intron"
FT   exon            616. .720
FT                   /*tag= c
FT                   /number= 2
FT                   /note= "putative exon"
FT   intron          721. .963
FT                   /*tag= d
FT                   /number= 2
FT                   /note= "putative intron"
FT   exon            964. .1203
FT                   /*tag= e
FT                   /number= 3
FT                   /note= "putative exon"
XX
PN   US5942393-A.
XX
PD   24-AUG-1999.
XX
PF   18-DEC-1996;   96US-00772113.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Takabayashi K,  Carson DA,  Nobori T;
XX
DR   WPI; 1999-507775/42.
XX
PT   Detecting catalytically active and inactive methylthioadenosine
PT   phosphorylase (MTAse) in mammalian cells useful for identifying malignant
PT   cells which are suitable targets for methionine (MET) starvation therapy.
XX
PS   Claim 6; Fig 1; 14pp; English.
XX
CC   This invention describes a novel method for detecting catalytically
CC   active and inactive methylthioadenosine phosphorylase (MTAse) in
CC   mammalian cells, using oligonucleotide probes which hybridize to MTAse
CC   nucleic acid coding regions. Detection of MTAse encoding nucleic acid
CC   indicates the cell has catalytically active MTAse. The method is useful
CC   for detecting malignant cells with a deficient MTAse gene, useful for
CC   identifying malignant cells which are suitable targets for methionine
CC   (MET) starvation therapy. The new method is simple, efficient and
CC   successful at determining MTAse negative cells, unlike prior art
```

```
CC   techniques, which include analysis of catalytic activity in cell
CC   cultures, requiring a commercially unavailable radiochemical substrate,
CC   and immunoassays, using MTAse antibodies which are unable to be produced
CC   in sufficient quantities. Recombinant MTAse protein produced using the
CC   new polynucleotide and vector, allows greater and purer production of
CC   MTAse than prior art techniques (using the Rangione method) for isolating
CC   native MTAse. This sequence represents human MTAse encoding DNA which is
CC   used in the method of the invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 7
AAF86091
ID   AAF86091 standard; DNA; 2763 BP.
XX
AC   AAF86091;
XX
DT   06-JUL-2001  (first entry)
XX
DE   Methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW   cancer; ds.
XX
OS   Unidentified.
XX
PN   US6214571-B1.
XX
PD   10-APR-2001.
XX
PF   24-NOV-1998;   98US-00199137.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 2001-315458/33.
XX
PT   Inhibiting adenine succinate synthetase (ASS) activity in
PT   methylthioadenosine phosphorylase deficient cells of mammalian host
PT   involves administering ASS inhibitor which depletes adenosine 5'
PT   monophosphate in cells.
XX
PS   Disclosure; Fig 1; 17pp; English.
XX
CC   The present invention relates to inhibiting adenyl succinate synthetase
CC   (ASS) activity in methylthioadenosine phosphorylase (MTAse) deficient
CC   cells of mammalian host. The invention may be used as a treatment for
CC   cancer, especially breest and colon cancer
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 123;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 8
AAD64097
ID   AAD64097 standard; DNA; 2763 BP.
XX
AC   AAD64097;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human methylthioadenosine phosphorylase (MTAse) genomic DNA.
XX
KW   Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW   CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTAse;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  a
FT   intron          422. .615
FT                   /*tag=  b
FT   exon            616. .720
FT                   /*tag=  c
FT   intron          721. .963
FT                   /*tag=  d
FT   exon            964. .1203
FT                   /*tag=  e
XX
PN   US2003138928-A1.
XX
PD   24-JUL-2003.
XX
PF   18-JUL-2001; 2001US-00908671.
XX
PR   26-AUG-1997;   97US-00921954.
XX
PA   (CARS/) CARSON D A.
PA   (NOBO/) NOBORI T.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 2003-851737/79.
XX
PT   New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
PT   for preparing a composition for diagnosing or treating cancer.
XX
PS   Example 1; SEQ ID NO 14; 46pp; English.
XX
CC   The present invention relates to novel tumour suppressor genes, termed as
CC   cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC   proteins. The polynucleotides are useful for preparing a composition for
CC   diagnosing or treating cancer. Sequences of the invention are also useful
CC   in gene therapy. The present sequence is human methylthioadenosine
CC   phosphorylase (MTAse) genomic DNA used in the exemplification of the
CC   invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;
```

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  Query Match            100.0%;  Score 123;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 9
AAQ99202
ID   AAQ99202 standard; DNA; 2784 BP.
XX
AC   AAQ99202;
XX
DT   07-MAR-1996  (first entry)
XX
DE   Pseudomonas putida methylthioadenosine-phosphorylase DNA.
XX
KW   Enzyme; MTAase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW   chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS   Pseudomonas putida.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2763
FT                   /*tag=  a
XX
PN   WO9517908-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014919.
XX
PR   29-DEC-1993;   93US-00176413.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Nobori T,  Carson DA;
XX
DR   WPI; 1995-246192/32.
XX
PT   Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT   negative tumour cells - used in chemotherapy of mammalian malignant
PT   cells.
XX
PS   Disclosure; Page 27-28; 46pp; English.
XX
CC   Antigenic peptides may be generated from this sequence encoding
CC   methyladenosine-phosphorylase, which are then used to generate antibodies
CC   specific for MTAse. The produced antibodies may be used in an immunoassay
CC   for the detection of MTase
XX
SQ   Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

  Query Match            100.0%;  Score 123;  DB 2;  Length 2784;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 10
AAX58284
ID   AAX58284 standard; DNA; 3083 BP.
XX
AC   AAX58284;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Human methylthioadenosine phosphorylase genomic DNA.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             119. .2876
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   exon            119. .151
FT                   /*tag=  b
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag=  c
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag=  d
FT                   /number= 2
FT   intron          537. .723
FT                   /*tag=  e
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag=  f
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag=  g
FT                   /number= 3
FT   exon            899. .1067
FT                   /*tag=  h
FT                   /number= 4
FT   intron          1068. .1377
FT                   /*tag=  i
FT                   /number= 4
FT   exon            1378. .1480
FT                   /*tag=  j
FT                   /number= 5
FT   intron          1481. .1763
FT                   /*tag=  k
FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag=  l
FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag=  m
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag=  n
FT                   /number= 7
FT   intron          2549. .2837
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FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag=  p
FT                   /number= 8
XX
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PN   WO9920791-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022557.
XX
PR   23-OCT-1997;   97US-00956657.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Cottam HB,  Nobori T,  Carrera CJ;
XX
DR   WPI; 1999-302753/25.
XX
PT   Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT   leukemia's.
XX
PS   Example 3; Page 42-44; 45pp; English.
XX
CC   This is the DNA sequence of a human methylthioadenosine phosphorylase
CC   (MTAse) genomic DNA clone that was isolated from a cosmid gene library
CC   using an MTAse cDNA probe. The encoded enzyme catabolises
CC   methylthioadenosine to adenine for endogenous salvage incorporation into
CC   the intracellular AMP pool. The invention relates to methods for treating
CC   and preventing the onset and maintenance of multiple drug resistance
CC   (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC   cells are depleted of AMP and ATP and are thus unable to supprt P-
CC   glycoprotein activity. One method obtains a population of target cells
CC   from a host and assays for loss of MTAse activity. MTAse deficient cells
CC   are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC   starves the cells of adenine and suppresses P-glycoprotein activity. The
CC   MTAse deficient host cells are preferably primary tumour cells comprising
CC   small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC   cells or urothelial tumor cells, preferably in humans. MTAse competent
CC   cells are also treated for MDR with purine synthesis inhibitors. MTAse
CC   competent and deficient cells are also treated for malignancy with other
CC   anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC   to detect the presence or absence of MTAse in malignant cell lines
XX
SQ   Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;

  Query Match             100.0%;  Score 123;  DB 2;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-33;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||
Db       2546 AAG 2548


RESULT 11
ABX10818
ID   ABX10818 standard; DNA; 3083 BP.
XX
AC   ABX10818;
XX
DT   17-APR-2003  (first entry)
XX
DE   DNA encoding rat methylthioadenosine phosphorylase (MTAse).
XX
KW   Rat; methylthioadenosine phosphorylase; MTAse; detection;
KW   Rangione method; gene; ds.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   exon            119. .151
FT                   /*tag= a
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag= b
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag= a
FT                   /number= 2
FT   intron          537. .723
FT                   /*tag= b
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag= a
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag= b
FT                   /number= 3
FT   exon            899. .1066
FT                   /*tag= a
FT                   /number= 4
FT   intron          1067. .1377
FT                   /*tag= b
FT                   /number= 4
FT   exon            1378. .1480
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FT                   /number= 5
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FT                   /*tag= b
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag= a
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag= b
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag= a
FT                   /number= 8
XX
PN   US2002146695-A1.
XX
PD   10-OCT-2002.
XX
PF   09-FEB-2001; 2001US-00780114.
XX
PR   29-DEC-1993;   93US-00176855.
PR   02-JUN-1995;   95US-00459343.
PR   04-MAY-1998;   98US-00072914.
XX
PA   (NOBO/) NOBORI T.
PA   (CARS/) CARSON D A.
PA   (TAKA/) TAKABAYASHI K.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 2003-208976/20.
XX
PT   Detection of methylthioadenosine phosphorylase presence in mammalian
PT   cells, by adding to sample oligonucleotide probes capable of hybridizing
PT   to methylthioadenosine phosphorylase encoding nucleic acid.
XX
PS   Claim 7; Fig 1; 16pp; English.
XX
CC   The invention describes a method of detecting methylthioadenosine
CC   phosphorylase (MTAse) comprising adding oligonucleotide probes
```

CC hybridisable to MTAse encoding nucleic acid to an assayable sample of
CC cells, where the presence of the nucleic acid indicates the presence of
CC the MTAse in a cell. The inventive method is simple and efficient in
CC detecting the presence of MTAse in the mammalian cell. The availability
CC of the recombinant MTAse enables the production of highly pure material
CC with greater ease and in greater quantities than was obtained using
CC Rangione method for the isolation and purification of native MTAse. This
CC sequence encodes rat methylthioadenosine phosphorylase (MTAse)
XX
SQ Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

Query Match 100.0%; Score 123; DB 8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||
Db       2546 AAG 2548
```

RESULT 12
AAH33683
ID AAH33683 standard; cDNA; 1437 BP.
XX
AC AAH33683;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:739.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 9; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG74252.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 1; Page 2728-2729; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 1437 BP; 501 A; 202 C; 262 G; 460 T; 0 U; 12 Other;

Query Match 91.9%; Score 113; DB 4; Length 1437;
Best Local Similarity 95.0%; Pred. No. 6.9e-30;
Matches 113; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy          5 CGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGC 64
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Db          1 CGGTGTACCGTGTCTTAAAGCCCCTGAAAGAWAACGCTAATAAMGCCAAAAGCTTACTGC 60

Qy         65 TCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTGAAG 123
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Db         61 TCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCMTAACCTGAAG 119
```

RESULT 13
ABQ59125
ID ABQ59125 standard; cDNA; 662 BP.
XX
AC ABQ59125;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:2820.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiaglingam A, Lewis ME;
XX
DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate

```
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists
XX
SQ   Sequence 662 BP; 171 A; 134 C; 148 G; 165 T; 0 U; 44 Other;

  Query Match             33.5%;  Score 41.2;  DB 6;  Length 662;
  Best Local Similarity   71.3%;  Pred. No. 0.00023;
  Matches   87;  Conservative    0;  Mismatches   30;  Indels    5;  Gaps    3;

Qy          2 TTTCGGTGGACCGGGTCTTAAAGACCCTGAAAG--AAAACGCTAATAAAGCCA-AAAGCT 58
              || |||||||||||||| |||||  ||||| |||  ||| ||||  |||| ||| ||||||
Db        444 TTCCGGTGGACCGGGTNTTAAANGCCCTGGAAGGAAAACCGCTNTTAAANCCATAAAGCT 503

Qy         59 TACTGCTCACTACCA--TACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAA 116
              || || ||  |  ||    |  |||||||||| ||| |||||||   ||  |  | |||
Db        504 TANTGNTCNATTACAATACCTNNAGATAGGGTCNACAAAATGGTCCANAAAACCTCNTAA 563

Qy        117 CC 118
              ||
Db        564 CC 565


RESULT 14
ABQ59540/c
ID   ABQ59540 standard; cDNA; 603 BP.
XX
AC   ABQ59540;
XX
DT   02-AUG-2002  (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:3235.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030732.
XX
PR   02-OCT-2000; 2000US-0237271P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Burgess C,  Astle JH,  Carroll E,  Catino TJ,  Dwivedi P,  Molino GA;
PI   Thiaglingam A,  Lewis ME;
XX
DR   WPI; 2002-426115/45.
XX
PT   New isolated nucleic acid that is differentially expressed in cancer
PT   tissues useful for determining the presence of colon cancer in a cell or
PT   tissue type, and in antisense therapy.
XX
PS   Claim 1; Fig 1; 796pp; English.
XX
CC   ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC   encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC   used in antisense therapy. An antibody immunoreactive with a polypeptide
CC   encoded by (I) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide encoded by a
CC   nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC   from (I) can be used for determining the presence of a nucleic acid which
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists
XX
SQ   Sequence 603 BP; 159 A; 119 C; 110 G; 206 T; 0 U; 9 Other;

  Query Match             25.4%;  Score 31.2;  DB 6;  Length 603;
  Best Local Similarity   70.9%;  Pred. No. 0.84;
  Matches   39;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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              |||||||||| |||||| || ||   ||| |||  ||||| | |  ||  | |||
Db        567 GTTTCGGTGGCCCGGGTTTTTAANGNCCTTAAAAGAAACGNTTAATAAAGCCAAA 513


RESULT 15
ABL69213/c
ID   ABL69213 standard; DNA; 145831 BP.
XX
AC   ABL69213;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Prostate cancer related gene sequence SEQ ID NO:7550.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
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PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 7550; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;

Query Match 25.2%; Score 31; DB 6; Length 145831;
Best Local Similarity 68.3%; Pred. No. 6.4;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy         121 AAG 123
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Db        9240 ATG 9238
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Job time : 163.422 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 35.927 Seconds
(without alignments)
2433.465 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGGACCGGGTCTT.....AAACCCTCCATAACCTGAAG 123

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	123	100.0	499	4	US-09-621-976-17307	Sequence 17307, A
	2	123	100.0	2763	1	US-08-176-413-1	Sequence 1, Appli
	3	123	100.0	2763	2	US-08-612-542B-1	Sequence 1, Appli
	4	123	100.0	2763	2	US-08-772-113-1	Sequence 1, Appli
	5	123	100.0	2763	3	US-09-199-137-1	Sequence 1, Appli
	6	123	100.0	2763	4	US-08-227-800A-14	Sequence 14, Appl
	7	123	100.0	2763	4	US-08-921-954-14	Sequence 14, Appl
	8	123	100.0	2763	5	PCT-US94-14919-1	Sequence 1, Appli
	9	123	100.0	2763	5	PCT-US94-14920-1	Sequence 1, Appli
	10	123	100.0	3083	3	US-08-956-657-1	Sequence 1, Appli
	11	123	100.0	3083	4	US-09-335-231-25	Sequence 25, Appl
c	12	30.4	24.7	796	4	US-09-270-767-5941	Sequence 5941, Ap
c	13	30.4	24.7	796	4	US-09-270-767-21223	Sequence 21223, A
	14	28	22.8	2736	3	US-09-235-451-3	Sequence 3, Appli
	15	28	22.8	2736	4	US-09-978-303-3	Sequence 3, Appli
	16	27.2	22.1	1143	4	US-09-248-796A-5559	Sequence 5559, Ap
c	17	27	22.0	1025	4	US-09-270-767-4982	Sequence 4982, Ap
c	18	27	22.0	1025	4	US-09-270-767-20264	Sequence 20264, A
	19	26.8	21.8	584	4	US-09-404-879A-268	Sequence 268, App
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	21	26.8	21.8	584	4	US-09-215-681-268	Sequence 268, App
	22	26.8	21.8	584	4	US-09-216-003A-268	Sequence 268, App
	23	26.8	21.8	584	4	US-09-667-857-268	Sequence 268, App
	24	26.6	21.6	1224	4	US-09-248-796A-5483	Sequence 5483, Ap
c	25	26.2	21.3	8106	3	US-09-135-241-1	Sequence 1, Appli
c	26	26	21.1	6669	4	US-10-204-708-6	Sequence 6, Appli
c	27	25.8	21.0	12847	1	US-08-550-715-1	Sequence 1, Appli
	28	25.8	21.0	44453	3	US-09-146-053-5	Sequence 5, Appli
	29	25.4	20.7	195	4	US-09-328-352-1949	Sequence 1949, Ap
	30	25.4	20.7	699	4	US-09-583-110-1893	Sequence 1893, Ap
c	31	25.4	20.7	733	3	US-08-998-416-1027	Sequence 1027, Ap
c	32	25.4	20.7	1209	4	US-09-328-352-1076	Sequence 1076, Ap
c	33	25.4	20.7	5501	4	US-10-204-708-38	Sequence 38, Appl
	34	25.4	20.7	10851	2	US-08-286-819A-16	Sequence 16, Appl
	35	25.4	20.7	10851	3	US-08-980-357-16	Sequence 16, Appl
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c	37	25.2	20.5	480	4	US-09-134-000C-1596	Sequence 1596, Ap
c	38	25.2	20.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
c	39	25.2	20.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
c	40	25.2	20.5	246240	2	US-08-724-394A-22	Sequence 22, Appl
c	41	25	20.3	443	4	US-09-513-999C-24786	Sequence 24786, A
c	42	25	20.3	1369	3	US-08-695-191-15	Sequence 15, Appl
c	43	25	20.3	1369	3	US-08-682-080-15	Sequence 15, Appl
	44	25	20.3	1400	2	US-08-481-658B-43	Sequence 43, Appl
	45	25	20.3	1400	2	US-08-477-504A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17307
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17307

Query Match 100.0%; Score 123; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        236 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 295

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Qy        121 AAG 123
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Db        356 AAG 358
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RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500

```
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  90067
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/176,413
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Howells, Stacy L.
;       REGISTRATION NUMBER:  34,842
;       REFERENCE/DOCKET NUMBER:  PD2864
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 455-5100
;       TELEFAX:  (619) 455-5110
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2763 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     IMMEDIATE SOURCE:
;       CLONE:  methyladenosine phosphatase
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2763
US-08-176-413-1

  Query Match             100.0%;  Score 123;  DB 1;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 3
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
;  GENERAL INFORMATION:
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    APPLICANT:  No. 5840505ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    TITLE OF INVENTION:  METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
;    TITLE OF INVENTION:  ACTIVITY IN MALIGNANT METHYLTHIOADENOSINE PHOSPHORYLASE DEFICI
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,542B
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-612-542B-1

  Query Match             100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 4
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5942393ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Takabayashi, Kenji
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/772,113
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
```

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;      APPLICATION NUMBER:  US/08/176,855
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-772-113-1

  Query Match             100.0%;  Score 123;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 5
US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6214571ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,137
;      FILING DATE:  24-NOV-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-09-199-137-1

  Query Match             100.0%;  Score 123;  DB 3;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 6
US-08-227-800A-14
; Sequence 14, Application US/08227800A
; Patent No. 6689561
;  GENERAL INFORMATION:
;    APPLICANT:  CARSON, DENNIS A.
;    APPLICANT:  NOBORI, TSUTOMU
;    TITLE OF INVENTION:  TUMOR SUPPRESSOR GENE AND METHODS FOR
;    TITLE OF INVENTION:  DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANC
;    TITLE OF INVENTION:  TREATMENT
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,800A
;      FILING DATE:  14-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOWELLS, STACY L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/023001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Methylthioadenosine Phosphorylase (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-227-800A-14

  Query Match             100.0%;  Score 123;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 7
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
;   GENERAL INFORMATION:
;        APPLICANT: Carson, Dennis A.
;                   No. 6689864ori, Tsutomu
;        TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
;                            Detection of Cancer, Monitoring of Tumor Progression and
;                            Cancer Treatment
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/921,954
;             FILING DATE: 26-Aug-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671A
;             FILING DATE: 18-Jul-2001
;             APPLICATION NUMBER: US 08/921,954
;             FILING DATE: 20-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hinsch, Matthew E.
;             REGISTRATION NUMBER: 47,651
;             REFERENCE/DOCKET NUMBER: 02307O-104042US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  1..2763
;             OTHER INFORMATION:  /note= "full-length
;             methylthioadenosine phosphorylase
;             (MTAse) genomic nucleotide sequence"
;        FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  254..421
;        FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  616..720
;        FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  964..1203
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

  Query Match             100.0%;  Score 123;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 8
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR SELECTIVE METHIONINE
;    TITLE OF INVENTION:  STARVATION OF MALIGNANT CELLS IN MAMMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14919
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-286
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     IMMEDIATE SOURCE:
;       CLONE:  methyladenosine phosphatase
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2763
PCT-US94-14919-1

  Query Match             100.0%;  Score 123;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 9
PCT-US94-14920-1
; Sequence 1, Application PC/TUS9414920
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14920
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-287
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14920-1

  Query Match             100.0%;  Score 123;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1640 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
              |||
Db       1760 AAG 1762


RESULT 10
US-08-956-657-1
; Sequence 1, Application US/08956657
; Patent No. 6210917
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6210917ori et al., Tsutomu
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/956,657
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/827,342
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Taylor, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/050001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3083 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-956-657-1

  Query Match             100.0%;  Score 123;  DB 3;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-34;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485
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Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||
Db       2546 AAG 2548
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RESULT 11
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 02307O-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTAP) gene
; NAME/KEY: modified_base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
US-09-335-231-25

Query Match 100.0%; Score 123; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
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RESULT 12
US-09-270-767-5941/c
; Sequence 5941, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5941
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5941

Query Match 24.7%; Score 30.4; DB 4; Length 796;
Best Local Similarity 57.3%; Pred. No. 0.22;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          19 TTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTACCATACCT 78
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RESULT 13
US-09-270-767-21223/c
; Sequence 21223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21223
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-21223

Query Match 24.7%; Score 30.4; DB 4; Length 796;
Best Local Similarity 57.3%; Pred. No. 0.22;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy          19 TTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTACCATACCT 78
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Db         193 TTGCAACCACATAAAATATATATAAATTTAAGCAAAAGCTTACTCACCAGAACGATACCT 134

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RESULT 14
US-09-235-451-3
; Sequence 3, Application US/09235451
; GENERAL INFORMATION:

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;  APPLICANT: Julius, David J.
;  APPLICANT:  Caterina, Michael J.
;  APPLICANT:  Brake, Anthony J.
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
;  TITLE OF INVENTION:  CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
;  TITLE OF INVENTION:  POLYPEPTIDES AND USES THEREOF
;  FILE REFERENCE: 9076/084CIP
;  CURRENT APPLICATION NUMBER: US/09/235,451
;  CURRENT FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER: 60/072,151
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 08/915,461
;  PRIOR FILING DATE: 1997-08-20
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 2736
;   TYPE: DNA
;   ORGANISM: R. rattus
;   FEATURE:
US-09-235-451-3

  Query Match             22.8%;  Score 28;  DB 3;  Length 2736;
  Best Local Similarity   55.0%;  Pred. No. 2.5;
  Matches   55;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          11 ACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTA 70
               |||  | | | |   ||||||||  |  ||| ||  ||| ||||| |    |  |||
Db        1207 ACCAAGGCCTCACACCCCTGAAACTAGCCGCCAAGGAAGGCAAAATCGAGATTTTCAGGC 1266

Qy          71 CCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCT 110
                |||  |||   |  | | ||| |  ||   |  ||||
Db        1267 ACATTCTGCAGCGGGAATTCTCAGGACCGTACCAGCCCCT 1306


RESULT 15
US-09-978-303-3
; Sequence 3, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
;  APPLICANT: Julius, David J.
;  APPLICANT:  Caterina, Michael J.
;  APPLICANT:  Brake, Anthony J.
;  TITLE OF INVENTION: Nucleic acid sequences encoding
;  TITLE OF INVENTION:  capsaicin receptor and capsaicin receptor-related
;  TITLE OF INVENTION:  polypeptides and uses thereof
;  FILE REFERENCE: UCAL084CON
;  CURRENT APPLICATION NUMBER: US/09/978,303
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/235,451
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/072,151
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 08/915,461
;  PRIOR FILING DATE: 1997-08-20
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 2736
;   TYPE: DNA
;   ORGANISM: R. rattus
US-09-978-303-3

  Query Match             22.8%;  Score 28;  DB 4;  Length 2736;
  Best Local Similarity   55.0%;  Pred. No. 2.5;
  Matches   55;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          11 ACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTA 70
               |||  | | | |   ||||||||  |  ||| ||  ||| ||||| |    |  |||
Db        1207 ACCAAGGCCTCACACCCCTGAAACTAGCCGCCAAGGAAGGCAAAATCGAGATTTTCAGGC 1266

Qy          71 CCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCT 110
                |||  |||   |  | | ||| |  ||   |  ||||
Db        1267 ACATTCTGCAGCGGGAATTCTCAGGACCGTACCAGCCCCT 1306


Search completed: February  1, 2005, 15:01:05
Job time : 36.927 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 169.156 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGGACCGGGTCTT.....AAACCCTCCATAACCTGAAG 123

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	123	100.0	870	16	US-10-367-366-1	Sequence 1, Appli
2	123	100.0	2269	18	US-10-779-476-2	Sequence 2, Appli
3	123	100.0	2763	10	US-09-908-671-14	Sequence 14, Appl
4	123	100.0	3083	9	US-09-780-114-1	Sequence 1, Appli
5	123	100.0	3083	15	US-10-326-681-25	Sequence 25, Appl
6	113	91.9	1437	15	US-10-106-698-749	Sequence 749, App
7	41.2	33.5	662	11	US-09-969-034-2820	Sequence 2820, Ap
8	31.8	25.9	3186778	13	US-10-027-632-174961	Sequence 174961,
9	31.8	25.9	3186778	15	US-10-027-632-174961	Sequence 174961,
c 10	31.2	25.4	603	11	US-09-969-034-3235	Sequence 3235, Ap
c 11	31	25.2	145831	9	US-09-969-708-79	Sequence 79, Appl
c 12	31	25.2	145831	9	US-09-954-456-2116	Sequence 2116, Ap
c 13	31	25.2	145831	10	US-09-873-367C-646	Sequence 646, App
c 14	31	25.2	145831	11	US-09-968-007A-455	Sequence 455, App
c 15	31	25.2	145831	16	US-10-240-425-363	Sequence 363, App
c 16	29.8	24.2	760	18	US-10-363-345A-3575	Sequence 3575, Ap
17	29.8	24.2	760	18	US-10-363-345A-3576	Sequence 3576, Ap
c 18	29.2	23.7	2207	15	US-10-331-496A-84	Sequence 84, Appl
19	29.2	23.7	2940917	13	US-10-027-632-174763	Sequence 174763,
20	29.2	23.7	2940917	15	US-10-027-632-174763	Sequence 174763,
c 21	29	23.6	7746	15	US-10-311-455-1829	Sequence 1829, Ap
c 22	29	23.6	7746	16	US-10-257-166-129	Sequence 129, App
c 23	28.8	23.4	2891	15	US-10-080-381B-72	Sequence 72, Appl
24	28.8	23.4	211257	13	US-10-087-192-529	Sequence 529, App
25	28.6	23.3	237	18	US-10-425-115-174545	Sequence 174545,
c 26	28.6	23.3	339	18	US-10-425-115-148116	Sequence 148116,
27	28.4	23.1	499	13	US-10-027-632-310136	Sequence 310136,
28	28.4	23.1	499	15	US-10-027-632-310136	Sequence 310136,
c 29	28.4	23.1	14112	15	US-10-311-455-1415	Sequence 1415, Ap
c 30	28.4	23.1	14112	16	US-10-221-714A-199	Sequence 199, App
c 31	28.4	23.1	14112	17	US-10-433-793-9	Sequence 9, Appli
32	28.4	23.1	392112	18	US-10-812-232-3	Sequence 3, Appli
c 33	28.2	22.9	609	13	US-10-027-632-197273	Sequence 197273,
c 34	28.2	22.9	609	15	US-10-027-632-197273	Sequence 197273,
c 35	28.2	22.9	688	13	US-10-027-632-201264	Sequence 201264,
c 36	28.2	22.9	688	13	US-10-027-632-201265	Sequence 201265,
c 37	28.2	22.9	688	13	US-10-027-632-201266	Sequence 201266,
c 38	28.2	22.9	688	13	US-10-027-632-201267	Sequence 201267,
c 39	28.2	22.9	688	13	US-10-027-632-201268	Sequence 201268,
c 40	28.2	22.9	688	13	US-10-027-632-201269	Sequence 201269,
c 41	28.2	22.9	688	15	US-10-027-632-201264	Sequence 201264,
c 42	28.2	22.9	688	15	US-10-027-632-201265	Sequence 201265,
c 43	28.2	22.9	688	15	US-10-027-632-201266	Sequence 201266,
c 44	28.2	22.9	688	15	US-10-027-632-201267	Sequence 201267,
c 45	28.2	22.9	688	15	US-10-027-632-201268	Sequence 201268,

ALIGNMENTS

RESULT 1
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Pei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skalitzky , Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; TITLE OF INVENTION: Phosphorylase Deficient Cells
; FILE REFERENCE: PC19080A (AG110-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

Query Match 100.0%; Score 123; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 816

Qy        121 AAG 123
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Db        817 AAG 819


RESULT 2
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
;  APPLICANT: Salmedix, Inc.
;  APPLICANT:  Leoni,Lorenzo M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
;  TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
;  FILE REFERENCE: 076936-0307942
;  CURRENT APPLICATION NUMBER: US/10/779,476
;  CURRENT FILING DATE:  2004-02-13
;  PRIOR APPLICATION NUMBER: 60/447,888
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: 60/460,715
;  PRIOR FILING DATE: 2004-04-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-779-476-2

  Query Match             100.0%;  Score 123;  DB 18;  Length 2269;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        812 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 871

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db        872 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 931

Qy        121 AAG 123
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Db        932 AAG 934


RESULT 3
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
;   GENERAL INFORMATION:
;        APPLICANT: CARSON, DENNIS A.
;                   NOBORI, TSUTOMU
;        TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
;                            DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
;                            TREATMENT
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: California
;             COUNTRY: US
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671
;             FILING DATE: 18-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/227,800
;             FILING DATE: 14-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HOWELLS, STACY L.
;             REGISTRATION NUMBER: 34,842
;             REFERENCE/DOCKET NUMBER: 07340/023001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
;             TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        IMMEDIATE SOURCE:
;             CLONE: Methylthioadenosine Phosphorylase (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..2763
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

  Query Match             100.0%;  Score 123;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db       1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 1759

Qy        121 AAG 123
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Db       1760 AAG 1762


RESULT 4
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020146695A1ori, Tsutomu
;                   Carson, Dennis A.
;                   Takabayashi, Kenji
;        TITLE OF INVENTION: Method for Detection of the Presence or
;                            Absence of Methylthioadenosine Phosphorylase
;                            (MTAse) in a
;                            Cell Sample by Detection of the Presence or Absence
;        NUMBER OF SEQUENCES: 1
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
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;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/780,114
;            FILING DATE: 09-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/072,914
;            FILING DATE: 04-May-1998
;            APPLICATION NUMBER: US 08/176,855
;            FILING DATE: 29-DEC-1993
;            APPLICATION NUMBER: US 08/459,343
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 08/827,342
;            FILING DATE: 26-MAR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bastian, Kevin L.
;            REGISTRATION NUMBER: 34,774
;            REFERENCE/DOCKET NUMBER: 02307O-103030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3083 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..3083
;            OTHER INFORMATION:  /note= "rat methylthioadenosine
;            phosphorylase (MTAse)"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  119..151
;            OTHER INFORMATION:  /note= "exon 1"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  450..536
;            OTHER INFORMATION:  /note= "exon 2"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  724..782
;            OTHER INFORMATION:  /note= "exon 3"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  899..1066
;            OTHER INFORMATION:  /note= "exon 4"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1378..1480
;            OTHER INFORMATION:  /note= "exon 5"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1764..1953
;            OTHER INFORMATION:  /note= "exon 6"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2426..2548
;            OTHER INFORMATION:  /note= "exon 7"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2838..2876
;            OTHER INFORMATION:  /note= "exon 8"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

  Query Match             100.0%;  Score 123;  DB 9;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||

Db       2546 AAG 2548


RESULT 5
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE: 02307O-108010US
;  CURRENT APPLICATION NUMBER: US/10/326,681
;  CURRENT FILING DATE:  2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/090,411
;  PRIOR FILING DATE: 1998-06-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-10-326-681-25
```

```
  Query Match             100.0%;  Score 123;  DB 15;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-31;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2545

Qy        121 AAG 123
              |||
Db       2546 AAG 2548


RESULT 6
US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-106-698-749

  Query Match             91.9%;  Score 113;  DB 15;  Length 1437;
  Best Local Similarity   95.0%;  Pred. No. 5.2e-28;
  Matches  113;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACTGC 64
              ||||| |||| ||||||||| ||||||||||:||||||||||:||||||||||||||||
Db          1 CGGTGTACCGTGTCTTAAAGCCCCTGAAAGAWAACGCTAATAAMGCCAAAAGCTTACTGC 60

Qy         65 TCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTGAAG 123
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db         61 TCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCMTAACCTGAAG 119


RESULT 7
US-09-969-034-2820
; Sequence 2820, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT:  Astle, Jon H.
;  APPLICANT:  Carroll, Eddie III
;  APPLICANT:  Catino, Theodore J.
;  APPLICANT:  Dwivedi, Poornima
;  APPLICANT:  Molino, Gary A.
;  APPLICANT:  Thiagalingam, Arunthathi
;  APPLICANT:  Lewis, Marcia E.
;  TITLE OF INVENTION: Nucleic Acid Sequences Differentially
;  TITLE OF INVENTION:  Expressed in Cancer Tissue
;  FILE REFERENCE: 1657/1032
;  CURRENT APPLICATION NUMBER: US/09/969,034
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: 60/237,271
;  PRIOR FILING DATE: 2000-02-10
;  NUMBER OF SEQ ID NOS: 4494
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2820
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 51, 127, 216, 234, 235, 240, 289, 315, 338, 362, 365, 390,
;   LOCATION: 402, 405, 410, 411, 432, 436, 442, 460, 466, 487, 493, 506,
;   LOCATION: 509, 512, 525, 526, 537, 551, 560, 566, 570, 576, 581, 583,
;   LOCATION: 588, 609, 611, 621, 632, 636, 649, 657
;   OTHER INFORMATION: n = A,T,C or G
US-09-969-034-2820

  Query Match             33.5%;  Score 41.2;  DB 11;  Length 662;
  Best Local Similarity   71.3%;  Pred. No. 0.00099;
  Matches   87;  Conservative    0;  Mismatches   30;  Indels    5;  Gaps    3;

Qy          2 TTTCGGTGGACCGGGTCTTAAAGACCCTGAAAG--AAAACGCTAATAAAGCCA-AAAGCT 58
              || ||||||||||||| |||||  ||||| |||  ||| ||||  |||| ||| ||||||
Db        444 TTCCGGTGGACCGGGTNTTAAANGCCCTGGAAGGAAAACCGCTNTTAAANCCATAAAGCT 503

Qy         59 TACTGCTCACTACCA--TACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAA 116
              || || ||  |  ||    |  ||||||||| ||| |||||||   ||  |  | |||
Db        504 TANTGNTCNATTACAATACCTNNAGATAGGGTCNACAAAATGGTCCANAAAACCTCNTAA 563

Qy        117 CC 118
              ||
Db        564 CC 565


RESULT 8
US-10-027-632-174961
; Sequence 174961, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174961
;   LENGTH: 3186778
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3186778)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961

  Query Match             25.9%;  Score 31.8;  DB 13;  Length 3186778;
  Best Local Similarity   58.1%;  Pred. No. 21;
```

```
  Matches   54;  Conservative    1;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          3 TTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACT 62
              |||| | | |||| | ||        :  |  ||||| | |  ||| ||||||||  |
Db    1986449 TTCGATAGTCCGGTTATTGGTACTAAKTGATTAAAACTCCATGAAATCCAAAAGCCCATA 1986508

Qy         63 GCTCACTACCATACCTCAGATAGGGTCCACAGA 95
              | |||| || |||  ||    ||||||   |||
Db    1986509 GATCACAACAATAAGTCCACCAGGGTCGGGAGA 1986541


RESULT 9
US-10-027-632-174961
; Sequence 174961, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174961
;   LENGTH: 3186778
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3186778)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961

  Query Match             25.9%;  Score 31.8;  DB 15;  Length 3186778;
  Best Local Similarity   58.1%;  Pred. No. 21;
  Matches   54;  Conservative    1;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          3 TTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTACT 62
              |||| | | |||| | ||        :  |  ||||| | |  ||| ||||||||  |
Db    1986449 TTCGATAGTCCGGTTATTGGTACTAAKTGATTAAAACTCCATGAAATCCAAAAGCCCATA 1986508

Qy         63 GCTCACTACCATACCTCAGATAGGGTCCACAGA 95
              | |||| || |||  ||    ||||||   |||
Db    1986509 GATCACAACAATAAGTCCACCAGGGTCGGGAGA 1986541


RESULT 10
US-09-969-034-3235/c
; Sequence 3235, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT:  Astle, Jon H.
;  APPLICANT:  Carroll, Eddie III
;  APPLICANT:  Catino, Theodore J.
;  APPLICANT:  Dwivedi, Poornima
;  APPLICANT:  Molino, Gary A.
;  APPLICANT:  Thiagalingam, Arunthathi
;  APPLICANT:  Lewis, Marcia E.
;  TITLE OF INVENTION: Nucleic Acid Sequences Differentially
;  TITLE OF INVENTION:  Expressed in Cancer Tissue
;  FILE REFERENCE: 1657/1032
;  CURRENT APPLICATION NUMBER: US/09/969,034
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: 60/237,271
;  PRIOR FILING DATE: 2000-02-10
;  NUMBER OF SEQ ID NOS: 4494
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3235
;   LENGTH: 603
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 492, 497, 506, 527, 542, 544, 573, 576, 597
;   OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235

  Query Match             25.4%;  Score 31.2;  DB 11;  Length 603;
  Best Local Similarity   70.9%;  Pred. No. 2.4;
  Matches   39;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAA 55
              |||||||||| |||||| || ||   ||| |||  ||||| | |  ||  | |||
Db        567 GTTTCGGTGGCCCGGGTTTTTAANGNCCTTAAAAGAAACGNTTAATAAAGCCAAA 513


RESULT 11
US-09-969-708-79/c
; Sequence 79, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
;  APPLICANT: Augustus, Meena
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signati
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-70
;  CURRENT APPLICATION NUMBER: US/09/969,708
;  CURRENT FILING DATE:  2001-10-03
;  PRIOR APPLICATION NUMBER: US/60/237,606
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: US/60/237,608
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: US/60/237,425
;  PRIOR FILING DATE: 2000-10-03
;  NUMBER OF SEQ ID NOS: 658
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
;   LENGTH: 145831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-969-708-79

  Query Match             25.2%;  Score 31;  DB 9;  Length 145831;
  Best Local Similarity   68.3%;  Pred. No. 15;
  Matches   43;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              | ||| ||| ||| |||||    |||||  |||||  ||  |||||  | ||| |||  ||
Db       9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAGCACTCAATATTCTC 9241

Qy        121 AAG 123
              | ||
Db       9240 ATG 9238


RESULT 12
US-09-954-456-2116/c
; Sequence 2116, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
```

```
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2116
;   LENGTH: 145831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-2116

  Query Match             25.2%;  Score 31;  DB 9;  Length 145831;
  Best Local Similarity   68.3%;  Pred. No. 15;
  Matches   43;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
               | ||| ||| ||| |||||    |||||  ||||| ||  |||||  | ||| |||  ||
Db        9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAGCACTCAATATTCTC 9241

Qy         121 AAG 123
               | |
Db        9240 ATG 9238


RESULT 13
US-09-873-367C-646/c
; Sequence 646, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  APPLICANT:  Soppet, Daniel
;  APPLICANT:  Endress, Gregory
;  APPLICANT:  Augustus, Meena
;  APPLICANT:  Ebner, Reinhard
;  APPLICANT:  Carter, Kenneth
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-64
;  CURRENT APPLICATION NUMBER: US/09/873,367C
;  CURRENT FILING DATE:  2003-04-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,891
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,842
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/244,867
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: U.S. 60/245,084
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 1067
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 646
;   LENGTH: 145831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-873-367C-646

  Query Match             25.2%;  Score 31;  DB 10;  Length 145831;
  Best Local Similarity   68.3%;  Pred. No. 15;
  Matches   43;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
               | ||| ||| ||| |||||    |||||  ||||| ||  |||||  | ||| |||  ||
Db        9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAGCACTCAATATTCTC 9241

Qy         121 AAG 123
               | |
Db        9240 ATG 9238


RESULT 14
US-09-968-007A-455/c
; Sequence 455, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signa
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-71
;  CURRENT APPLICATION NUMBER: US/09/968,007A
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,172
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,173
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,278
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,294
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,295
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,316
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 1001
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 455
;   LENGTH: 145831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-007A-455

  Query Match             25.2%;  Score 31;  DB 11;  Length 145831;
  Best Local Similarity   68.3%;  Pred. No. 15;
  Matches   43;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
               | ||| ||| ||| |||||    |||||  ||||| ||  |||||  | ||| |||  ||
Db        9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAGCACTCAATATTCTC 9241

Qy         121 AAG 123
               | |
Db        9240 ATG 9238


RESULT 15
US-10-240-425-363/c
; Sequence 363, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Amanda
;  APPLICANT:  Boland, Joseph F.
;  APPLICANT:  Lord, Reginald V.
;  APPLICANT:  Alvarez, Chris
;  APPLICANT:  Wetzel, Jon C.
;  APPLICANT:  Scherf, Uwe
```

```
;  APPLICANT:  Vockley, Joseph G.
;  TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;  FILE REFERENCE: 44921-5026
;  CURRENT APPLICATION NUMBER: US/10/240,425
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: PCT/US01/09847
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/193,446
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 1588
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 363
;   LENGTH: 145831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF001548
US-10-240-425-363

  Query Match             25.2%;  Score 31;  DB 16;  Length 145831;
  Best Local Similarity   68.3%;  Pred. No. 15;
  Matches   43;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
               | ||| ||| ||| |||||    |||||  ||||| ||  |||||  | ||| |||  ||
Db        9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAGCACTCAATATTCTC 9241

Qy         121 AAG 123
               | |
Db        9240 ATG 9238


Search completed: February  1, 2005, 17:20:44
Job time : 181.156 secs
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 1382.94 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGGACCGGGTCTT.....AAACCCTCCATAACCTGAAG 123

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	123	100.0	570	6	CD364939	CD364939 UI-H-FT2-
	2	123	100.0	612	7	CN409515	CN409515 170006001
	3	123	100.0	638	7	CN409513	CN409513 170005327
	4	123	100.0	681	4	BM784030	BM784030 K-EST0062
c	5	123	100.0	684	6	CD364946	CD364946 UI-H-FT2-
	6	123	100.0	774	2	BE538925	BE538925 601061292
	7	123	100.0	813	9	AY405891	AY405891 Homo sapi
	8	123	100.0	836	1	AL048242	AL048242 DKFZp586O
	9	123	100.0	975	4	BM472910	BM472910 AGENCOURT
	10	123	100.0	1064	5	BX459089	BX459089 BX459089
	11	123	100.0	1380	3	BC012316	BC012316 Homo sapi
c	12	123	100.0	3028	3	HSM808193	BX648047 Homo sapi
c	13	121.4	98.7	205	2	BF431095	BF431095 7o07b11.x
c	14	121.4	98.7	257	1	AI919501	AI919501 tp22b01.x
	15	121.4	98.7	728	4	BG501032	BG501032 602546438
	16	119.4	97.1	580	4	BM839857	BM839857 K-EST0116
	17	119.4	97.1	580	4	BM840883	BM840883 K-EST0118
c	18	118.8	96.6	903	5	BX371508	BX371508 BX371508
c	19	118	95.9	330	5	BX102948	BX102948 BX102948
	20	118	95.9	562	7	CN409511	CN409511 170006000
c	21	116.6	94.8	911	5	BX350035	BX350035 BX350035
	22	113.4	92.2	1047	4	BM925551	BM925551 AGENCOURT
	23	112.4	91.4	813	9	AY405892	AY405892 Pan trogl
c	24	112	91.1	491	1	AA635142	AA635142 af10e10.s
	25	111	90.2	819	2	BF981023	BF981023 602310222
	26	110.4	89.8	1075	1	AL543068	AL543068 AL543068
c	27	110.2	89.6	429	1	AV667881	AV667881 AV667881
	28	110.2	89.6	477	4	BG938257	BG938257 1Abo14E09
	29	110.2	89.6	484	7	CF930825	CF930825 CF--05-R-
	30	110.2	89.6	562	4	BI774611	BI774611 466793 MA
c	31	110.2	89.6	581	6	CB538214	CB538214 776179 MA
	32	110.2	89.6	586	7	CN441464	CN441464 BE04026A1
c	33	110.2	89.6	600	7	CO701132	CO701132 DG32-195b
	34	110.2	89.6	682	7	CN788377	CN788377 4122709 B
	35	110.2	89.6	950	7	CF413058	CF413058 CH3#083_G
c	36	107.6	87.5	568	7	CO586973	CO586973 DG2-139I1
	37	106.6	86.7	692	7	CK968775	CK968775 4084058 B
	38	105.4	85.7	421	1	AJ667166	AJ667166 AJ667166
c	39	103	83.7	401	1	AI674711	AI674711 wd19e10.x
c	40	100.6	81.8	679	2	AW150875	AW150875 xg41d10.x
	41	99	80.5	885	5	BX374675	BX374675 BX374675
	42	95.8	77.9	303	6	CA535795	CA535795 C0224B10-
	43	95.8	77.9	443	6	CA536077	CA536077 C0228H03-
	44	95.8	77.9	488	1	AA939482	AA939482 vz50b06.r
	45	95.8	77.9	541	6	CA533816	CA533816 C0406H10-

ALIGNMENTS

RESULT 1
CD364939/c
LOCUS CD364939 570 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bjn-i-17-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.
ACCESSION CD364939
VERSION CD364939.1 GI:31149029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-i-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library

construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 7.4e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        527 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 468

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 408

Qy        121 AAG 123
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Db        407 AAG 405
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RESULT 2
CN409515
LOCUS CN409515 612 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600188932 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409515
VERSION CN409515.1 GI:47396639
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 612)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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source 1. .612
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN

Query Match 100.0%; Score 123; DB 7; Length 612;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        107 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 166

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 226

Qy        121 AAG 123
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Db        227 AAG 229
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RESULT 3
CN409513
LOCUS CN409513 638 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409513
VERSION CN409513.1 GI:47396637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 638)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 638 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Query Match 100.0%; Score 123; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 527

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 587

Qy        121 AAG 123
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Db        588 AAG 590


RESULT 4
BM784030
LOCUS       BM784030                681 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0062086 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-F01 5',
            mRNA sequence.
ACCESSION   BM784030
VERSION     BM784030.1  GI:19132262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 32  row: F  column: 01
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S6SNU620-32-F01"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Scattering floating"
                     /cell_line="SNU-620"
                     /lab_host="Top10F'"
                     /clone_lib="S6SNU620"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             100.0%;  Score 123;  DB 4;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        189 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 248

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db        249 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 308

Qy        121 AAG 123


              |||
Db        309 AAG 311


RESULT 5
CD364946/c
LOCUS       CD364946                684 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT2-bjn-k-07-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjn-k-07-0-UI 3', mRNA sequence.
ACCESSION   CD364946
VERSION     CD364946.1  GI:31149036
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjn-k-07-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella  moi 10, 24 hours; Staph
                     aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
                     Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
                     adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
                     hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
                     wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
                     The library was subtracted according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. The tissue
                     was provided by Dr. Gary W. Hunninghake of the University
                     of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT2
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 6;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db        467 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 408

Qy        121 AAG 123
              |||
Db        407 AAG 405


RESULT 6
BE538925
LOCUS       BE538925                774 bp    mRNA    linear   EST 09-AUG-2000
DEFINITION  601061292F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447622 5',
            mRNA sequence.
ACCESSION   BE538925
VERSION     BE538925.1  GI:9767570
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8421  row: h  column: 23
            High quality sequence stop: 615.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_10"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
ORIGIN

  Query Match            100.0%;  Score 123;  DB 2;  Length 774;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        127 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 186

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
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Db        187 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 246

Qy        121 AAG 123
              |||
Db        247 AAG 249


RESULT 7
AY405891
LOCUS       AY405891                813 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens MTAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY405891
VERSION     AY405891.1  GI:39761865
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 813)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .813
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>813
                     /gene="MTAP"
                     /locus_tag="HCM2375"
ORIGIN

  Query Match            100.0%;  Score 123;  DB 9;  Length 813;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 750

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 810

Qy        121 AAG 123
              |||
Db        811 AAG 813


RESULT 8
AL048242
LOCUS       AL048242                836 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp586O1023_r1 586 (synonym: hute1) Homo sapiens cDNA clone
            DKFZp586O1023, mRNA sequence.
ACCESSION   AL048242
VERSION     AL048242.1  GI:4729075
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Ansorge, et al.)
```

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp586O1023) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp586O1023"
                     /tissue_type="uterus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="586 (synonym: hute1)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 1;  Length 836;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 257

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 317

Qy        121 AAG 123
              |||
Db        318 AAG 320


RESULT 9
BM472910
LOCUS       BM472910                975 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6466233 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574548
            5', mRNA sequence.
ACCESSION   BM472910
VERSION     BM472910.1  GI:18521952
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 975)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12323  row: f  column: 21
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
     source          1. .975
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5574548"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 123;  DB 4;  Length 975;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 225

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 285

Qy        121 AAG 123
              |||
Db        286 AAG 288


RESULT 10
BX459089
LOCUS       BX459089                1064 bp    mRNA    linear   EST 06-MAY-2004
DEFINITION  BX459089 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YH01
            5-PRIME, mRNA sequence.
ACCESSION   BX459089
VERSION     BX459089.2  GI:47066799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1064)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 22, 2003 this sequence version replaced gi:31029072.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE012CD01QP1&c=5445.f.
FEATURES             Location/Qualifiers
     source          1. .1064
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE012YH01"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
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```
ORIGIN

  Query Match             100.0%;  Score 123;  DB 5;  Length 1064;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 719

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 779

Qy        121 AAG 123
              |||
Db        780 AAG 782


RESULT 11
BC012316
LOCUS       BC012316                1380 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone
            IMAGE:3546198), containing frame-shift errors.
ACCESSION   BC012316
VERSION     BC012316.1  GI:15147365
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1380)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1380)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 8 Row: b Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006025
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .1380
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3546198"
                     /tissue_type="Placenta, choriocarcinoma"
                     /clone_lib="NIH_MGC_21"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 3;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 854

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        855 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 914

Qy        121 AAG 123
              |||
Db        915 AAG 917


RESULT 12
HSM808193/c
LOCUS       HSM808193               3028 bp    mRNA    linear   HTC 03-AUG-2004
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686O20193 (from clone DKFZp686O20193).
ACCESSION   BX648047
VERSION     BX648047.1  GI:34367206
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3028)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686O20193) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686O20193
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
```

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     source          1. .3028
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686O20193"
                     /tissue_type="esophagus tumor"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
                     /note="unclassified"
ORIGIN

  Query Match             100.0%;  Score 123;  DB 3;  Length 3028;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-29;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2627 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2568

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2567 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 2508

Qy        121 AAG 123
              |||
Db       2507 AAG 2505


RESULT 13
BF431095/c
LOCUS       BF431095                205 bp    mRNA    linear   EST 29-NOV-2000
DEFINITION  7o07b11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3573452 3'
            similar to SW:MTAP_HUMAN Q13126 5'-METHYLTHIOADENOSINE
            PHOSPHORYLASE ;, mRNA sequence.
ACCESSION   BF431095
VERSION     BF431095.1  GI:11443209
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 205)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .205
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3573452"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Kid11"
                      /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                      prepared, and ss circles were made in vitro. Following HAP
                      purification, this DNA was used as tracer in a subtractive
                      hybridization reaction. The driver was PCR-amplified cDNAs
                      from a pool of 5,000 clones made from the same library
                      (cloneIDs 1322376-1323911, 1456007-1456775, and
                      1500552-1502855). Subtraction by Bento Soares and M.
                      Fatima Bonaldo.  "
ORIGIN

  Query Match             98.7%;  Score 121.4;  DB 2;  Length 205;
  Best Local Similarity   99.2%;  Pred. No. 2e-28;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        157 GTTTCGGTGGACCGGGTATTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 98

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 38

Qy        121 AAG 123
              |||
Db         37 AAG 35


RESULT 14
AI919501/c
LOCUS       AI919501                257 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tp22b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188489 3'
            similar to SW:MTAP_HUMAN Q13126 5'-METHYLTHIOADENOSINE
            PHOSPHORYLASE ;, mRNA sequence.
ACCESSION   AI919501
VERSION     AI919501.1  GI:5639356
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 257)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1521   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 246.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2188489"
                      /tissue_type="poorly differentiated adenocarcinoma with
                      signet ring cell features"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Gas4"
                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.69 kb. Life Technologies catalog #:
                      11549-011"
ORIGIN

  Query Match             98.7%;  Score 121.4;  DB 1;  Length 257;
  Best Local Similarity   99.2%;  Pred. No. 2.1e-28;
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  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        242 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTTATAAAGCCAAAAGCTTA 183

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 123

Qy        121 AAG 123
              |||
Db        122 AAG 120


RESULT 15
BG501032
LOCUS       BG501032                728 bp    mRNA    linear   EST 27-MAR-2001
DEFINITION  602546438F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668825 5',
            mRNA sequence.
ACCESSION   BG501032
VERSION     BG501032.1  GI:13462549
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1479  row: 1  column: 10
            High quality sequence stop: 722.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4668825"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_60"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.5
                     kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             98.7%;  Score 121.4;  DB 4;  Length 728;
  Best Local Similarity   99.2%;  Pred. No. 2.5e-28;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
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Db        489 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 548

Qy         61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCCTCCATAACCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAAGCCTCCATAACCTG 608

Qy        121 AAG 123
              |||
Db        609 AAG 611


Search completed: February  1, 2005, 14:58:30
Job time : 1383.94 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 1067.55 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGGAATTTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	190	100.0	567	9	AH013410S6	L42632 Homo sapien
2	190	100.0	849	9	CR541710	CR541710 Homo sapi
3	190	100.0	852	9	CR541670	CR541670 Homo sapi
4	190	100.0	870	6	AX826996	AX826996 Sequence
5	190	100.0	1021	9	L40432	L40432 Homo sapien
6	190	100.0	1450	6	AR474055	AR474055 Sequence
7	190	100.0	2269	9	HSU22233	U22233 Human methy
8	190	100.0	2763	6	AR059583	AR059583 Sequence
9	190	100.0	2763	6	I28320	I28320 Sequence 1
10	190	100.0	2763	6	AR473576	AR473576 Sequence
11	190	100.0	2763	6	AR474046	AR474046 Sequence
12	190	100.0	3083	6	AR144466	AR144466 Sequence
13	190	100.0	3083	6	AR342446	AR342446 Sequence
14	190	100.0	168656	9	AL359922	AL359922 Human DNA
15	190	100.0	250000	9	AB060808	AB060808 Homo sapi
16	188.4	99.2	1890	9	BC026106	BC026106 Homo sapi
17	164.4	86.5	807	9	L42635	L42635 Homo sapien
c 18	164.4	86.5	94125	9	AC016966	AC016966 Homo sapi
c 19	164.4	86.5	168366	2	AC069409	AC069409 Homo sapi
c 20	164.4	86.5	180606	2	AC073406	AC073406 Homo sapi
21	154.8	81.5	1055	10	AB056100	AB056100 Mus muscu
22	154.8	81.5	2565	10	BC003858	BC003858 Mus muscu
c 23	154.8	81.5	194025	10	AL831719	AL831719 Mouse DNA
c 24	148.4	78.1	225782	2	AC109529	AC109529 Rattus no
c 25	148.4	78.1	287775	2	AC108638	AC108638 Rattus no
26	119	62.6	441	6	CQ461249	CQ461249 Sequence
27	106.8	56.2	1255	5	BC056545	BC056545 Danio rer
28	106.8	56.2	1265	5	BC046035	BC046035 Danio rer
c 29	106.8	56.2	150073	5	BX323448	BX323448 Zebrafish
30	106.8	56.2	161859	2	CR385087	CR385087 Danio rer
31	97	51.1	339	9	AF216650	AF216650 Homo sapi
32	96.6	50.8	230762	2	AC097556	AC097556 Rattus no
c 33	96.6	50.8	232771	2	AC128406	AC128406 Rattus no
c 34	94.2	49.6	170899	2	AC144208	AC144208 Macaca mu
35	86.8	45.7	1193	6	CQ581994	CQ581994 Sequence
36	86.8	45.7	1227	3	BT004912	BT004912 Drosophil
c 37	86.8	45.7	3322	6	CQ581993	CQ581993 Sequence
c 38	86.8	45.7	3511	6	CQ586454	CQ586454 Sequence
c 39	86.8	45.7	52465	2	AC020084	AC020084 Drosophil
40	86.8	45.7	161244	3	AC009535	AC009535 Drosophil
41	86.8	45.7	175506	3	AC008004	AC008004 Drosophil
42	86.8	45.7	290783	3	AE003803	AE003803 Drosophil
43	75.8	39.9	90801	9	AC025033	AC025033 Homo sapi
c 44	75.8	39.9	146349	2	AC012027	AC012027 Homo sapi
c 45	75.8	39.9	171615	2	AC089988	AC089988 Homo sapi

ALIGNMENTS

RESULT 1
AH013410S6
LOCUS AH013410S6 567 bp DNA linear PRI 01-DEC-2003
DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 6.
ACCESSION L42632
VERSION L42632.1 GI:38570312
KEYWORDS .
SEGMENT 6 of 8
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 567)
AUTHORS Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.
TITLE Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
MEDLINE 96234115
PUBMED 8650244
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="P1-267"
/tissue_type="placenta"
exon 64. .303
/gene="MTAP"
/note="putative"
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ORIGIN

Query Match 100.0%; Score 190; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 64 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 123

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Qy          61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 183

Qy         121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 243

Qy         181 TGTTACGCAA 190
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Db         244 TGTTACGCAA 253


RESULT 2
CR541710
LOCUS       CR541710                849 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834H1128D for
            gene MTAP, methylthioadenosine phosphorylase; complete cds, without
            stopcodon.
ACCESSION   CR541710
VERSION     CR541710.1  GI:49456380
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 849)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834H1128D, ORFNo 3404
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834H1128D RZPDLIB;
            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            Clone name at Harvard Institute of Proteomics
            (www.hip.harvard.edu): FLH131058.01L
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned without stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence NM_002451 (GI:6006025) we found
            AA exchange(s) at position (first base of changed triplet):
            133(leu->ser) 166(ile->val)
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES             Location/Qualifiers
     source          1. .849
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RZPDo834H1128D"
                     /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                     /lab_host="DH5Alpha"
                     /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene            1. .849
                     /gene="MTAP"
     CDS             1. .>849
                     /gene="MTAP"
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                     /protein_id="CAG46511.1"
                     /db_xref="GI:49456381"
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                     SILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
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                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 9;  Length 849;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 510

Qy          61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         571 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 630

Qy         181 TGTTACGCAA 190
               ||||||||||
Db         631 TGTTACGCAA 640


RESULT 3
CR541670
LOCUS       CR541670                852 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens full open reading frame cDNA clone RZPDo834G1127D for
            gene MTAP, methylthioadenosine phosphorylase; complete cds, incl.
            stopcodon.
ACCESSION   CR541670
VERSION     CR541670.1  GI:49456300
KEYWORDS    Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 852)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Cloning of human full open reading frames in Gateway(TM) system
            entry vector (pDONR201)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 852)
  AUTHORS   Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
            Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
            Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
            Germany
COMMENT     RZPD; RZPDo834G1127D, ORFNo 3305
            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834G1127D RZPDLIB;
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            Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
            834
            www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
            www.rzpd.de/products/orfclones/
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available from RZPD;
            Contact RZPD (customer.service@rzpd.de) for further information.
            This CDS clone is part of a collection of human full ORF clones
            jointly established and verified by the Harvard Institute of
            Proteomics (HIP) and RZPD.
            This CDS has been cloned incl. stopcodon.
            The CDS has been inserted into pDONR201 via a BP Clonase(TM)
            reaction. Additional sequence has been added in front of the start
            codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
            The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att
            The clone is validated by full sequence check.
            Compared to the reference sequence NM_002451 (GI:6006025) we found
            AA exchange(s) at position (first base of changed triplet):
            139(leu->met) 166(ile->val)
            Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES                Location/Qualifiers
     source             1. .852
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="RZPDo834G1127D"
                        /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
                        /lab_host="DH5Alpha"
                        /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
     gene               1. .852
                        /gene="MTAP"
     CDS                1. .852
                        /gene="MTAP"
                        /codon_start=1
                        /protein_id="CAG46471.1"
                        /db_xref="GI:49456301"
                        /translation="MASGTTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                        LIMGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
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                        LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                        TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                        SVLLPRH"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 9;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 510

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 570

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 630

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        631 TGTTACGCAA 640


RESULT 4
AX826996
LOCUS       AX826996                870 bp    DNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 1 from Patent WO03074083.
ACCESSION   AX826996
VERSION     AX826996.1  GI:39837205
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bloom,L.A., Boritzki,T.J., Kung,P.P., Ogden,R.C., Skalitzky,D.J.,
            Zehnder,L.R., Kuhn,L.A. and Meng,J.J.
  TITLE     Combination therapies for treating methylthioadenosine
            phosphorylase deficient cells
  JOURNAL   Patent: WO 03074083-A 1 12-SEP-2003;
            PFIZER INC. (US)
FEATURES                Location/Qualifiers
     source             1. .870
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Cloned MTAP cDNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 516

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 576

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 636

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        637 TGTTACGCAA 646


RESULT 5
L40432
LOCUS       L40432                  1021 bp    mRNA    linear   PRI 12-DEC-2000
DEFINITION  Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
            complete cds.
ACCESSION   L40432
VERSION     L40432.1  GI:11602391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Genomic cloning of methylthioadenosine phosphorylase: a purine
            metabolic enzyme deficient in multiple different cancers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
  MEDLINE   96234115
   PUBMED   8650244
REFERENCE   2  (bases 1 to 1021)
  AUTHORS   Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
            Research on Aging, and Department of Medicine, University of
            California at San Diego, La Jolla, CA 92093-0663, USA
COMMENT     GSDB:S:39613.
            [Flatfile retrieved from GSDB Thu Dec  7 15:18:48 2000].
FEATURES                Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p22-p21"
                     /tissue_type="placenta"
                     /tissue_lib="lambda gt11"
     gene            1. .1021
                     /gene="MTAP"
     CDS             111. .962
                     /gene="MTAP"
                     /EC_number="2.4.2.28"
                     /note="putative"
                     /codon_start=1
                     /product="methylthioadenosine phosphorylase"
                     /protein_id="AAG38871.1"
                     /db_xref="GI:11602392"
                     /translation="MASGTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMG
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 190;  DB 9;  Length 1021;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 620

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 680

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 740

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        741 TGTTACGCAA 750


RESULT 6
AR474055
LOCUS       AR474055               1450 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 23 from patent US 6689864.
ACCESSION   AR474055
VERSION     AR474055.1  GI:42712808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1450)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Cyclin dependent kinase 4 inhibitor
  JOURNAL   Patent: US 6689864-A 23 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .1450
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 190;  DB 6;  Length 1450;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 7
HSU22233
LOCUS       HSU22233               2269 bp    mRNA    linear   PRI 25-NOV-1995
DEFINITION  Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.
ACCESSION   U22233
VERSION     U22233.1  GI:847723
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2269)
  AUTHORS   Olopade,O.I., Pomykala,H.M., Hagos,F., Sveen,L.W., Espinosa,R. III,
            Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and
            Bohlander,S.K.
  TITLE     Construction of a 2.8-megabase yeast artificial chromosome contig
            and cloning of the human methylthioadenosine phosphorylase gene
            from the tumor suppressor region on 9p21
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
  MEDLINE   95327672
   PUBMED   7604019
REFERENCE   2  (bases 1 to 2269)
  AUTHORS   Olopade,O.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,
            University of Chicago Pritzker School of Medicine, 5841 S. Maryland
            Avenue, Chicago, IL 60637-1470, USA
FEATURES             Location/Qualifiers
     source          1. .2269
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p21"
                     /clone="18-11 cDNA"
                     /sex="male"
                     /cell_line="primary culture"
                     /cell_type="fibroblast"
                     /tissue_type="epidermis"
     gene            1. .2269
                     /gene="MTAP"
     CDS             122. .973
                     /gene="MTAP"
                     /codon_start=1
                     /product="methylthioadenosine phosphorylase"
                     /protein_id="AAA81646.1"
                     /db_xref="GI:847724"
                     /translation="MASGTTTAVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDA
                     LILGKIKNVDCILLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEI
                     QPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLG
                     LRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMA
                     TDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQF
                     SVLLPRH"
ORIGIN

  Query Match           100.0%;  Score 190;  DB 9;  Length 2269;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 631

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 691

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 751

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        752 TGTTACGCAA 761


RESULT 8
AR059583
LOCUS       AR059583                2763 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5840505.
ACCESSION   AR059583
VERSION     AR059583.1  GI:5986033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
  TITLE     Method for inhibiting adenylosuccinate synthetase activity in
            methylthioadenosine phosphorylase deficient cells
  JOURNAL   Patent: US 5840505-A 1 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 9
I28320
LOCUS       I28320                  2763 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5571510.
ACCESSION   I28320
VERSION     I28320.1  GI:1819096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Nobori,T. and Carson,D.A.
  TITLE     Method for selective methionine starvation of malignant cells in
            mammals
  JOURNAL   Patent: US 5571510-A 1 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 10
AR473576
LOCUS       AR473576                2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689561.
ACCESSION   AR473576
VERSION     AR473576.1  GI:42711901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Tumor suppressor gene and methods for detection of cancer,
            monitoring of tumor progression and cancer treatment
  JOURNAL   Patent: US 6689561-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 11
AR474046
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LOCUS       AR474046               2763 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6689864.
ACCESSION   AR474046
VERSION     AR474046.1  GI:42712799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2763)
  AUTHORS   Carson,D.A. and Nobori,T.
  TITLE     Cyclin dependent kinase 4 inhibitor
  JOURNAL   Patent: US 6689864-A 14 10-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .2763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 12
AR144466
LOCUS       AR144466               3083 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6210917.
ACCESSION   AR144466
VERSION     AR144466.1  GI:15106333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A. and Carrera,C.J.
  TITLE     Method for suppressing multiple drug resistance in cancer cells
  JOURNAL   Patent: US 6210917-A 1 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .3083
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 13
AR342446
LOCUS       AR342446               3083 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 25 from patent US 6576420.
ACCESSION   AR342446
VERSION     AR342446.1  GI:33737456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3083)
  AUTHORS   Carson,D.A., Schmid,M. and Carrera,C.J.
  TITLE     Method for early diagnosis of, and determination of prognosis in,
            cancer
  JOURNAL   Patent: US 6576420-A 25 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .3083
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 6;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 14
AL359922
LOCUS       AL359922             168656 bp    DNA     linear   PRI 17-JAN-2001
DEFINITION  Human DNA sequence from clone RP11-70L8 on chromosome 9, complete
            sequence.
ACCESSION   AL359922
VERSION     AL359922.10  GI:12191425
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 168656)
  AUTHORS   Laird,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Jan 13, 2001 this sequence version replaced gi:11878000.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
```

only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-70L8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-70L8 The true left end of clone RP11-149I2 is at 118787 in this sequence. The true right end of clone RP11-473O3 is at 73731 in this sequence.

```
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /clone="RP11-70L8"
                     /clone_lib="RPCI-11.1"
     misc_feature    98399. .98416
                     /note="Single clone region. Assembly confirmed by
                     restriction digest data."
     misc_feature    98649. .98718
                     /note="Single clone region. Assembly confirmed by
                     restriction digest data."
     misc_feature    157251. .157348
                     /note="Single clone region. L1 repeat. Assembly confirmed
                     by restriction digest data"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.1e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112028 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 112087

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112088 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 112147

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112148 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 112207

Qy        181 TGTTACGCAA 190
              ||||||||||
Db     112208 TGTTACGCAA 112217


RESULT 15
AB060808
LOCUS       AB060808               250000 bp    DNA     linear   PRI 26-APR-2002
DEFINITION  Homo sapiens gene for p16/CDKN2A, complete cds.
ACCESSION   AB060808
VERSION     AB060808.1  GI:20330501
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kohno,T., Inoue,K., Kitagawa,Y., Hayashi,Y., Matsuo,Y.,
            Mizoguchi,H. and Yokota,J.
  TITLE     Prevalent Involvement of Illegitimate V(D)J Recombination in
            Chromosome 9p21 Deletions in Lymphoid Leukemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 250000)
  AUTHORS   Yokota,J., Kohno,T., Inoue,K. and Kitagawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2001) Takashi Kohno, National Cancer Center
            Research Institute, Biology Division; 1-1, Tsukiji 5-chome,
            Chuo-ku, Tokyo 104-0045, Japan (E-mail:tkkohno@gan2.res.ncc.go.jp,
            Tel:81-3-3542-2511(ex.4652), Fax:81-3-3542-0807)
FEATURES             Location/Qualifiers
     source          1. .250000
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9p21"
     gene            complement(join(185617. .185630,188290. .188596,
                     192072. .192221))
                     /gene="p16/CDKN2A"
     CDS             complement(join(185617. .185630,188290. .188596,
                     192072. .192221))
                     /gene="p16/CDKN2A"
                     /codon_start=1
                     /product="p16/CDKN2A"
                     /protein_id="BAB91133.1"
                     /db_xref="GI:20330502"
                     /translation="MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSY
                     GRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGA
                     RLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 9;  Length 250000;
  Best Local Similarity   100.0%;  Pred. No. 2e-49;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72028 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 72087

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72088 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 72147

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72148 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 72207

Qy        181 TGTTACGCAA 190
              ||||||||||
Db      72208 TGTTACGCAA 72217


Search completed: February  1, 2005, 13:26:02
Job time : 1069.55 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 249.351 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGGAATTTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	190	100.0	870	10	ADC37133	Adc37133 Cloned me
	2	190	100.0	2197	10	ADC30327	Adc30327 Human nov
	3	190	100.0	2763	2	AAT15167	Aat15167 Methylthi
	4	190	100.0	2763	2	AAQ92813	Aaq92813 Human MTA
	5	190	100.0	2763	2	AAT85305	Aat85305 Human met
	6	190	100.0	2763	2	AAZ00866	Aaz00866 Human MTA
	7	190	100.0	2763	5	AAF86091	Aaf86091 Methylthi
	8	190	100.0	2763	10	AAD64097	Aad64097 Human met
	9	190	100.0	2784	2	AAQ99202	Aaq99202 Pseudomon
	10	190	100.0	3083	2	AAX58284	Aax58284 Human met
	11	190	100.0	3083	8	ABX10818	Abx10818 DNA encod
	12	148	77.9	1419	10	AAD64106	Aad64106 CDK4I rel
	13	135.2	71.2	662	6	ABQ59125	Abq59125 Human col
	14	119	62.6	441	6	ABL81049	Abl81049 Human ova
	15	86.8	45.7	1193	4	ABL08341	Abl08341 Drosophil
c	16	86.8	45.7	3322	4	ABL08340	Abl08340 Drosophil
c	17	86.8	45.7	3511	4	ABL11314	Abl11314 Drosophil
	18	71.4	37.6	6461	4	ABL11024	Abl11024 Drosophil
	19	59.8	31.5	300	2	AAZ14961	Aaz14961 Human gen
c	20	59.6	31.4	110000	12	ADN46845_16	Continuation (17 o
c	21	59.6	31.4	110000	12	ADN46845_17	Continuation (18 o
	22	59.6	31.4	110000	12	ADN47591_03	Continuation (4 of
c	23	59.6	31.4	110000	12	ADN46123_16	Continuation (17 o
c	24	59.6	31.4	110000	12	ADN46123_17	Continuation (18 o
	25	59.6	31.4	110000	12	ADN47209_03	Continuation (4 of
c	26	59.6	31.4	110000	12	ADN46464_16	Continuation (17 o
c	27	59.6	31.4	110000	12	ADN46464_17	Continuation (18 o
	28	59.6	31.4	110000	12	ADN47960_03	Continuation (4 of
	29	58.8	30.9	790	2	AAZ16103	Aaz16103 Human gen
c	30	57.2	30.1	349980	5	AAH41225	Aah41225 Pyrococcu
	31	54.6	28.7	110000	4	AAI99682_06	Continuation (7 of
	32	54.6	28.7	110000	4	AAI99683_06	Continuation (7 of
	33	53.2	28.0	596	10	ADG38065	Adg38065 Aspergill
	34	53.2	28.0	1029	3	AAF14549	Aaf14549 Aspergill
c	35	50.2	26.4	349980	5	AAF86431	Aaf86431 Pyrococcu
c	36	47.8	25.2	110000	12	ADN46845_13	Continuation (14 o
	37	47.8	25.2	110000	12	ADN47591_07	Continuation (8 of
c	38	47.8	25.2	110000	12	ADN46123_13	Continuation (14 o
	39	47.8	25.2	110000	12	ADN47209_07	Continuation (8 of
c	40	47.8	25.2	110000	12	ADN46464_13	Continuation (14 o
	41	47.8	25.2	110000	12	ADN47960_07	Continuation (8 of
c	42	41	21.6	110000	11	ADM27081_00	Adm27081 Hyperther
	43	40	21.1	390	8	ABX41411	Abx41411 Bovine ES
	44	39.6	20.8	404	8	ABZ54499	Abz54499 Aspergill
c	45	36.6	19.3	602	8	ABZ52169	Abz52169 Aspergill

ALIGNMENTS

RESULT 1
ADC37133
ID ADC37133 standard; cDNA; 870 BP.
XX
AC ADC37133;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cloned methylthioadenosine phosphorylase, MTAP, cDNA.
XX
KW combination therapy; methylthioadenosine phosphorylase; MTAP; inhibitor;
KW glycinamide ribonucleotide formyltransferase; GARFT;
KW aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX
OS Unidentified.
XX
PN WO2003074083-A1.
XX
PD 12-SEP-2003.
XX
PF 17-FEB-2003; 2003WO-IB000615.
XX
PR 04-MAR-2002; 2002US-0361645P.
PR 09-DEC-2002; 2002US-0432275P.
XX
PA (PFIZ) PFIZER INC.
XX
PI Bloom LA, Boritzki TJ, Kung P, Ogden RC, Skalitzky DJ;
PI Zehnder LR, Kuhn LA, Meng JJ;
XX
DR WPI; 2003-748252/70.
XX
PT Selectively killing methylthioadenosine phosphorylase deficient cells
PT used for treating cell proliferative disorders comprises administering
PT glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX
PS Example 3B; Page 182-183; 189pp; English.
XX
CC This invention relates to novel combination therapies that selectively
CC kill methylthioadenosine phosphorylase (MTAP) deficient cells. The
CC combination therapies comprise administering an inhibitor of glycinamide

CC ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC toxicity agent during and after administration of the inhibitor. The
CC combination therapies can be used for selectively killing MTAP deficient
CC cells, and for treating cell proliferative disorders e.g. lung cancer,
CC leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC dose of the inhibitor. This polynucleotide sequence represents the cloned
CC MTAP cDNA of the invention.
XX
SQ Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 190; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
Db 457 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 516

Qy 61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
Db 517 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 576

Qy 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
Db 577 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 636

Qy 181 TGTTACGCAA 190
Db 637 TGTTACGCAA 646

RESULT 2
ADC30327
ID ADC30327 standard; cDNA; 2197 BP.
XX
AC ADC30327;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:409.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 3; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI; 2003-371981/35.
DR P-PSDB; ADC31298.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Claim 1; SEQ ID NO 409; 1185pp; English.
XX
CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of peventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Match 100.0%; Score 190; DB 10; Length 2197;
Best Local Similarity 100.0%; Pred. No. 2.2e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
Db 511 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 570

Qy 61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
Db 571 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 630

Qy 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
Db 631 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 690

Qy 181 TGTTACGCAA 190
Db 691 TGTTACGCAA 700

RESULT 3
AAT15167
ID AAT15167 standard; DNA; 2763 BP.
XX
AC AAT15167;
XX
DT 29-JUN-1996 (first entry)
XX
DE Methylthioadenosine-phosphorylase gene.
XX

```
KW   Human; methylthioadenosine-phosphorylase; chromosome walking;
KW   interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW   cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW   melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW   non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW   antibody; imaging; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= b
FT   intron          422. .615
FT                   /*tag= c
FT   exon            616. .720
FT                   /*tag= d
FT   intron          721. .963
FT                   /*tag= e
FT   exon            964. .1203
FT                   /*tag= f
XX
PN   WO9528169-A1.
XX
PD   26-OCT-1995.
XX
PF   12-APR-1995;   95WO-US004655.
XX
PR   14-APR-1994;   94US-00227800.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 1995-373630/48.
XX
PT   Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT   useful for diagnosis, assessing predisposition and treatment of cancers.
XX
PS   Example 1; Page 96-101; 129pp; English.
XX
CC   The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC   at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC   tumour suppressor gene (AAT15157-58) is located between this gene and an
CC   interferon-alpha gene cluster, and has been isolated by chromosome
CC   walking. The CDK4I gene, probe and primer derivatives and the gene
CC   product may be used in diagnosis of cancer, particularly melanoma
CC   (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC   carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC   or in antitumour antisense oligonucleotide or ribozyme construction.
CC   Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 190;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153
```

```
RESULT 4
AAQ92813
ID   AAQ92813 standard; DNA; 2763 BP.
XX
AC   AAQ92813;
XX
DT   25-MAR-2003  (revised)
DT   05-DEC-1995  (first entry)
XX
DE   Human MTAse.
XX
KW   MTAse; methyladenosine-phosphatase; malignancy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag= a
FT   exon            616. .720
FT                   /*tag= b
FT   exon            964. .1203
FT                   /*tag= c
FT   exon            1640. .1762
FT                   /*tag= d
FT   exon            2272. .2310
FT                   /*tag= e
XX
PN   WO9518233-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014920.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (CIBA ) CIBA GEIGY CORP.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 1995-246398/32.
XX
PT   Detecting methyl:adenosine phosphatase in mammalian cells - by
PT   hybridisation with specific oligonucleotide for detecting malignancy,
PT   also new nucleic acid, expression vectors, derived polypeptide(s) and
PT   antibodies.
XX
PS   Claim 8; Page 34-35; 47pp; English.
XX
CC   A cosmid gene library constructed from human placenta DNA was screened
CC   using a MTAse cDNA probe to isolate a human MTAse genomic clone (sequence
CC   given in AAQ92813). Absence of MTAse from a cell is indicative of
CC   malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 190;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143
```

```
Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 5
AAT85305
ID   AAT85305 standard; DNA; 2763 BP.
XX
AC   AAT85305;
XX
DT   28-FEB-1998  (first entry)
XX
DE   Human methylthioadenosine phosphorylase.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   adenylsuccinate synthetase; lung cancer; glioma;
KW   acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            254. .421
FT                   /*tag=  a
FT                   /number= 1
FT   intron          422. .615
FT                   /*tag=  b
FT                   /number= 1
FT   exon            616. .720
FT                   /*tag=  c
FT                   /number= 2
FT   intron          721. .963
FT                   /*tag=  d
FT                   /number= 2
FT   exon            964. .1203
FT                   /*tag=  e
FT                   /number= 3
XX
PN   WO9732994-A1.
XX
PD   12-SEP-1997.
XX
PF   27-JAN-1997;   97WO-US001193.
XX
PR   08-MAR-1996;   96US-00612542.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carrera CJ,  Carson DA,  Cottam HB,  Nobori T;
XX
DR   WPI; 1997-470550/43.
XX
PT   Inhibiting adenyl:succinate synthetase activity in methylthio:adenosine
PT   phosphorylase-deficient cells - by treatment with specific inhibitor,
PT   especially L-alanosine, useful for selective killing of MTAse deficient
PT   cancer cells.
XX
PS   Example 3; Page 25-26; 37pp; English.
XX
CC   This DNA sequence comprises human genomic DNA for methylthioadenosine
CC   phosphorylase (MTase), obtained from a cosmid gene library constructed
CC   from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC   method for inhibiting the activity adenylsuccinate synthetase (ASS) in
CC   mammalian cells deficient in MTAse activity involves: (a) determining
CC   that a population of cells obtained from a mammalian host is MTase
CC   deficient; and (b) administering an ASS inhibitor (preferably L-
CC   alanosine) to the host so that the MTase deficient host cells are
CC   depleted of AMP. The method is especially used to treat human MTAse-
CC   deficient primary tumour cells, specifically non-small cell lung cancer,
CC   acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC   MTAse catabolises methylthioadenosine to adenine for endogenous salvage
CC   incorporation into the intracellular AMP pool. The claimed method
CC   deprives the cells of substrate for de novo synthesis of AMP, resulting
CC   in selective killing of these cells. MTAse sequence-specific
CC   oligonuclotides can be used to detect the presence or absence of MTAse in
CC   malignant cell lines
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

  Query Match           100.0%;  Score 190;  DB 2;  Length 2763;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 6
AAZ00866
ID   AAZ00866 standard; DNA; 2763 BP.
XX
AC   AAZ00866;
XX
DT   20-OCT-1999  (first entry)
XX
DE   Human MTAse DNA.
XX
KW   MTAse; methylthioadenosine phosphorylase; human; detection; active;
KW   catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            253. .421
FT                   /*tag=  a
FT                   /number= 1
FT                   /note= "Putative exon"
FT   intron          422. .615
FT                   /*tag=  b
FT                   /number= 1
FT                   /note= "putative intron"
FT   exon            616. .720
FT                   /*tag=  c
FT                   /number= 2
FT                   /note= "putative exon"
FT   intron          721. .963
FT                   /*tag=  d
FT                   /number= 2
FT                   /note= "putative intron"
FT   exon            964. .1203
FT                   /*tag=  e
FT                   /number= 3
FT                   /note= "putative exon"
XX
PN   US5942393-A.
XX
PD   24-AUG-1999.
XX
PF   18-DEC-1996;   96US-00772113.
XX
PR   29-DEC-1993;   93US-00176855.
XX
PA   (REGC ) UNIV CALIFORNIA.
```

XX
PI Takabayashi K, Carson DA, Nobori T;
XX
DR WPI; 1999-507775/42.
XX
PT Detecting catalytically active and inactive methylthioadenosine
PT phosphorylase (MTAse) in mammalian cells useful for identifying malignant
PT cells which are suitable targets for methionine (MET) starvation therapy.
XX
PS Claim 6; Fig 1; 14pp; English.
XX
CC This invention describes a novel method for detecting catalytically
CC active and inactive methylthioadenosine phosphorylase (MTAse) in
CC mammalian cells, using oligonucleotide probes which hybridize to MTAse
CC nucleic acid coding regions. Detection of MTAse encoding nucleic acid
CC indicates the cell has catalytically active MTAse. The method is useful
CC for detecting malignant cells with a deficient MTAse gene, useful for
CC identifying malignant cells which are suitable targets for methionine
CC (MET) starvation therapy. The new method is simple, efficient and
CC successful at determining MTAse negative cells, unlike prior art
CC techniques, which include analysis of catalytic activity in cell
CC cultures, requiring a commercially unavailable radiochemical substrate,
CC and immunoassays, using MTAse antibodies which are unable to be produced
CC in sufficient quantities. Recombinant MTAse protein produced using the
CC new polynucleotide and vector, allows greater and purer production of
CC MTAse than prior art techniques (using the Rangione method) for isolating
CC native MTAse. This sequence represents human MTAse encoding DNA which is
CC used in the method of the invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy 61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
Db 1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
Db 1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy 181 TGTTACGCAA 190
Db 1144 TGTTACGCAA 1153

RESULT 7
AAF86091
ID AAF86091 standard; DNA; 2763 BP.
XX
AC AAF86091;
XX
DT 06-JUL-2001 (first entry)
XX
DE Methylthioadenosine phosphorylase.
XX
KW Methylthioadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW cancer; ds.
XX
OS Unidentified.
XX
PN US6214571-B1.
XX
PD 10-APR-2001.
XX
PF 24-NOV-1998; 98US-00199137.
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
DR WPI; 2001-315458/33.
XX
PT Inhibiting adenine succinate synthetase (ASS) activity in
PT methylthioadenosine phosphorylase deficient cells of mammalian host
PT involves administering ASS inhibitor which depletes adenosine 5'
PT monophosphate in cells.
XX
PS Disclosure; Fig 1; 17pp; English.
XX
CC The present invention relates to inhibiting adenyl succinate synthetase
CC (ASS) activity in methylthioadenosine phosphorylase (MTAse) deficient
CC cells of mammalian host. The invention may be used as a treatment for
CC cancer, especially breest and colon cancer
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 190; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy 61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
Db 1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
Db 1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy 181 TGTTACGCAA 190
Db 1144 TGTTACGCAA 1153

RESULT 8
AAD64097
ID AAD64097 standard; DNA; 2763 BP.
XX
AC AAD64097;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human methylthioadenosine phosphorylase (MTAse) genomic DNA.
XX
KW Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTAse;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254. .421
FT /*tag= a
FT intron 422. .615
FT /*tag= b
FT exon 616. .720
FT /*tag= c
FT intron 721. .963
FT /*tag= d
FT exon 964. .1203
FT /*tag= e
XX
PN US2003138928-A1.
XX

```
PD   24-JUL-2003.
XX
PF   18-JUL-2001; 2001US-00908671.
XX
PR   26-AUG-1997;   97US-00921954.
XX
PA   (CARS/) CARSON D A.
PA   (NOBO/) NOBORI T.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 2003-851737/79.
XX
PT   New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
PT   for preparing a composition for diagnosing or treating cancer.
XX
PS   Example 1; SEQ ID NO 14; 46pp; English.
XX
CC   The present invention relates to novel tumour suppressor genes, termed as
CC   cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC   proteins. The polynucleotides are useful for preparing a composition for
CC   diagnosing or treating cancer. Sequences of the invention are also useful
CC   in gene therapy. The present sequence is human methylthioadenosine
CC   phosphorylase (MTAse) genomic DNA used in the exemplification of the
CC   invention
XX
SQ   Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

  Query Match             100.0%;  Score 190;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 9
AAQ99202
ID   AAQ99202 standard; DNA; 2784 BP.
XX
AC   AAQ99202;
XX
DT   07-MAR-1996  (first entry)
XX
DE   Pseudomonas putida methylthioadenosine-phosphorylase DNA.
XX
KW   Enzyme; MTAase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW   chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS   Pseudomonas putida.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2763
FT                   /*tag=  a
XX
PN   WO9517908-A1.
XX
PD   06-JUL-1995.
XX
PF   22-DEC-1994;   94WO-US014919.
XX
PR   29-DEC-1993;   93US-00176413.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Nobori T,  Carson DA;
XX
DR   WPI; 1995-246192/32.
XX
PT   Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT   negative tumour cells - used in chemotherapy of mammalian malignant
PT   cells.
XX
PS   Disclosure; Page 27-28; 46pp; English.
XX
CC   Antigenic peptides may be generated from this sequence encoding
CC   methyladenosine-phosphorylase, which are then used to generate antibodies
CC   specific for MTAse. The produced antibodies may be used in an immunoassay
CC   for the detection of MTase
XX
SQ   Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

  Query Match             100.0%;  Score 190;  DB 2;  Length 2784;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 10
AAX58284
ID   AAX58284 standard; DNA; 3083 BP.
XX
AC   AAX58284;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Human methylthioadenosine phosphorylase genomic DNA.
XX
KW   Methylthioadenosine phosphorylase; MTAse; human;
KW   multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW   therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             119. .2876
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   exon            119. .151
FT                   /*tag=  b
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag=  c
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag=  d
FT                   /number= 2
FT   intron          537. .723
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```
FT                   /*tag= e
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag= f
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag= g
FT                   /number= 3
FT   exon            899. .1067
FT                   /*tag= h
FT                   /number= 4
FT   intron          1068. .1377
FT                   /*tag= i
FT                   /number= 4
FT   exon            1378. .1480
FT                   /*tag= j
FT                   /number= 5
FT   intron          1481. .1763
FT                   /*tag= k
FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag= l
FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag= m
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag= n
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag= o
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag= p
FT                   /number= 8
XX
PN   WO9920791-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022557.
XX
PR   23-OCT-1997;   97US-00956657.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Carson DA,  Cottam HB,  Nobori T,  Carrera CJ;
XX
DR   WPI; 1999-302753/25.
XX
PT   Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT   leukemia's.
XX
PS   Example 3; Page 42-44; 45pp; English.
XX
CC   This is the DNA sequence of a human methylthioadenosine phosphorylase
CC   (MTAse) genomic DNA clone that was isolated from a cosmid gene library
CC   using an MTAse cDNA probe. The encoded enzyme catabolises
CC   methylthioadenosine to adenine for endogenous salvage incorporation into
CC   the intracellular AMP pool. The invention relates to methods for treating
CC   and preventing the onset and maintenance of multiple drug resistance
CC   (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC   cells are depleted of AMP and ATP and are thus unable to supprt P-
CC   glycoprotein activity. One method obtains a population of target cells
CC   from a host and assays for loss of MTAse activity. MTAse deficient cells
CC   are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC   starves the cells of adenine and suppresses P-glycoprotein activity. The
CC   MTAse deficient host cells are preferably primary tumour cells comprising
CC   small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC   cells or urothelial tumor cells, preferably in humans. MTAse competent
CC   cells are also treated for MDR with purine synthesis inhibitors. MTAse
CC   competent and deficient cells are also treated for malignancy with other
CC   anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC   to detect the presence or absence of MTAse in malignant cell lines
XX
SQ   Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;

  Query Match           100.0%;  Score 190;  DB 2;  Length 3083;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 11
ABX10818
ID   ABX10818 standard; DNA; 3083 BP.
XX
AC   ABX10818;
XX
DT   17-APR-2003  (first entry)
XX
DE   DNA encoding rat methylthioadenosine phosphorylase (MTAse).
XX
KW   Rat; methylthioadenosine phosphorylase; MTAse; detection;
KW   Rangione method; gene; ds.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   exon            119. .151
FT                   /*tag= a
FT                   /number= 1
FT   intron          152. .449
FT                   /*tag= b
FT                   /number= 1
FT   exon            450. .536
FT                   /*tag= a
FT                   /number= 2
FT   intron          537. .723
FT                   /*tag= b
FT                   /number= 2
FT   exon            724. .782
FT                   /*tag= a
FT                   /number= 3
FT   intron          783. .898
FT                   /*tag= b
FT                   /number= 3
FT   exon            899. .1066
FT                   /*tag= a
FT                   /number= 4
FT   intron          1067. .1377
FT                   /*tag= b
FT                   /number= 4
FT   exon            1378. .1480
FT                   /*tag= a
FT                   /number= 5
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FT                   /number= 5
FT   exon            1764. .1953
FT                   /*tag= a
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FT                   /number= 6
FT   intron          1954. .2425
FT                   /*tag=  b
FT                   /number= 6
FT   exon            2426. .2548
FT                   /*tag=  a
FT                   /number= 7
FT   intron          2549. .2837
FT                   /*tag=  b
FT                   /number= 7
FT   exon            2838. .2876
FT                   /*tag=  a
FT                   /number= 8
XX
PN   US2002146695-A1.
XX
PD   10-OCT-2002.
XX
PF   09-FEB-2001; 2001US-00780114.
XX
PR   29-DEC-1993;   93US-00176855.
PR   02-JUN-1995;   95US-00459343.
PR   04-MAY-1998;   98US-00072914.
XX
PA   (NOBO/) NOBORI T.
PA   (CARS/) CARSON D A.
PA   (TAKA/) TAKABAYASHI K.
XX
PI   Nobori T,  Carson DA,  Takabayashi K;
XX
DR   WPI; 2003-208976/20.
XX
PT   Detection of methylthioadenosine phosphorylase presence in mammalian
PT   cells, by adding to sample oligonucleotide probes capable of hybridizing
PT   to methylthioadenosine phosphorylase encoding nucleic acid.
XX
PS   Claim 7; Fig 1; 16pp; English.
XX
CC   The invention describes a method of detecting methylthioadenosine
CC   phosphorylase (MTAse) comprising adding oligonucleotide probes
CC   hybridisable to MTAse encoding nucleic acid to an assayable sample of
CC   cells, where the presence of the nucleic acid indicates the presence of
CC   the MTAse in a cell. The inventive method is simple and efficient in
CC   detecting the presence of MTAse in the mammalian cell. The availability
CC   of the recombinant MTAse enables the production of highly pure material
CC   with greater ease and in greater quantities than was obtained using
CC   Rangione method for the isolation and purification of native MTAse. This
CC   sequence encodes rat methylthioadenosine phosphorylase (MTAse)
XX
SQ   Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

  Query Match            100.0%;  Score 190;  DB 8;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-55;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 12
```

```
AAD64106
ID   AAD64106 standard; DNA; 1419 BP.
XX
AC   AAD64106;
XX
DT   12-FEB-2004  (first entry)
XX
DE   CDK4I related DNA #9.
XX
KW   Tumour suppressor gene; cyclin-dependent kinase 4 inhibitor; CDK4I;
KW   cancer; gene therapy; ds.
XX
OS   Unidentified.
XX
PN   US2003138928-A1.
XX
PD   24-JUL-2003.
XX
PF   18-JUL-2001; 2001US-00908671.
XX
PR   26-AUG-1997;   97US-00921954.
XX
PA   (CARS/) CARSON D A.
PA   (NOBO/) NOBORI T.
XX
PI   Carson DA,  Nobori T;
XX
DR   WPI; 2003-851737/79.
XX
PT   New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
PT   for preparing a composition for diagnosing or treating cancer.
XX
PS   Disclosure; SEQ ID NO 23; 46pp; English.
XX
CC   The present invention relates to novel tumour suppressor genes, termed as
CC   cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC   proteins. The polynucleotides are useful for preparing a composition for
CC   diagnosing or treating cancer. Sequences of the invention are also useful
CC   in gene therapy. The present sequence is CDK4I related DNA
XX
SQ   Sequence 1419 BP; 368 A; 263 C; 340 G; 411 T; 0 U; 37 Other;

  Query Match            77.9%;  Score 148;  DB 10;  Length 1419;
  Best Local Similarity   96.8%;  Pred. No. 7.5e-41;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    3;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        949 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAA--GTC 1006

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1007 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCT--GGG 1064

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1065 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTG--ATT 1122

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1123 TGTTACGCAA 1132


RESULT 13
ABQ59125
ID   ABQ59125 standard; cDNA; 662 BP.
XX
AC   ABQ59125;
XX
DT   02-AUG-2002  (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:2820.
XX
```

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiaglingam A, Lewis ME;
XX
DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists
XX
SQ Sequence 662 BP; 171 A; 134 C; 148 G; 165 T; 0 U; 44 Other;

Query Match 71.2%; Score 135.2; DB 6; Length 662;
Best Local Similarity 90.1%; Pred. No. 1.6e-36;
Matches 173; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

```
Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              |||||||||||||||||||||| ||||||||||||||||  |||| ||||||||||||||
Db        194 GTTCTTATAGAGACTGCTAAGANGCTAGGACTCCGGTGCCNNTCAANGGGGACAATGGTC 253

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              |||||||||||||||| ||||||||||||    || |||||||||||||||||||||||
Db        254 ACAATCGAGGGACCTCG-TTTAGCTCCCGGCAGAAANGCTTCATGTTCCGCACCTGGGGG 312

Qy        121 GC-GGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCT-AAGGAGGCTGGAA 178
              || |||||||||||||||||||| || ||||||||| | ||||| || || |||||||
Db        313 GCNGGATGTTATCAACATGACCACANTTTCAGAGGTGGGTTTTGCTAAANGANGCTGGAA 372

Qy        179 TTTGTTACGCAA 190
              |||| |||||||
Db        373 TTTGATACGCAA 384
```

RESULT 14
ABL81049
ID ABL81049 standard; cDNA; 441 BP.
XX
AC ABL81049;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:4027.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017756.
XX
PR 26-MAY-2000; 2000US-0207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX
PS Claim 1; SEQ ID NO 4027; 489pp; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
CC or antigen presenting cells that express (II). (I) has cytostatic
CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
CC detecting ovarian cancer in a patient's biological sample preferably
CC serum or ovarian tissue. The method comprises contacting a biological
CC sample from a patient with (IV), detecting the amount of polynucleotide
CC hybridising to (IV) and comparing the amount to a predetermined cutoff
CC value and thereby detecting ovarian cancer in the patient, where the
CC amount of polynucleotide hybridising to (IV) is detected preferably by
CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC useful for stimulating and/or expanding T cells specific for an ovarian
CC tumour protein comprising contacting T cells with (III) or (II). (III) is
CC useful in design and preparation of ribozyme molecules for inhibiting
CC expression of the tumour polypeptides and proteins in tumour cells; and
CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
CC library using well known techniques
XX
SQ Sequence 441 BP; 115 A; 100 C; 118 G; 107 T; 0 U; 1 Other;

Query Match 62.6%; Score 119; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.1e-31;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 382

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 441
```

RESULT 15
ABL08341
ID ABL08341 standard; cDNA; 1193 BP.
XX
AC ABL08341;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19505.

XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB64238.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 19505; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1193 BP; 306 A; 294 C; 296 G; 297 T; 0 U; 0 Other;

Query Match 45.7%; Score 86.8; DB 4; Length 1193;
Best Local Similarity 66.7%; Pred. No. 1.4e-19;
Matches 124; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

```
Qy          2 TTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTCA 61
              ||||  |  || | || ||| |||| |   | |    ||||   ||||  || || || |
Db        793 TTCTGCTTCAGGCGGCCAAGGAGCTGGAGATTCCCGCCCACGATAAGGCCACCATTGTGA 852

Qy         62 CAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGGG 121
              | || ||||| || || ||   ||| ||  | || |||  |||||||||    ||||| |
Db        853 CTATTGAGGGTCCGCGCTTCTCCTCTCGCTCGGAGAGCCACATGTTCCGTCAGTGGGGCG 912

Qy        122 CGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATTT 181
               |||  | || ||||||||||   |||||| ||||| || || ||||||||||  |
Db        913 GGGACCTCATAAACATGACCACGTGTCCAGAAGTGGTGCTAGCCAAGGAGGCTGGCCTAC 972

Qy        182 GTTACG 187
              ||||||
Db        973 TTTACG 978
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Search completed: February 1, 2005, 12:39:41
Job time : 251.351 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 55.497 Seconds
(without alignments)
2433.465 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGGAATTTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	190	100.0	1450	4	US-08-921-954-23	Sequence 23, Appl
	2	190	100.0	2763	1	US-08-176-413-1	Sequence 1, Appli
	3	190	100.0	2763	2	US-08-612-542B-1	Sequence 1, Appli
	4	190	100.0	2763	2	US-08-772-113-1	Sequence 1, Appli
	5	190	100.0	2763	3	US-09-199-137-1	Sequence 1, Appli
	6	190	100.0	2763	4	US-08-227-800A-14	Sequence 14, Appl
	7	190	100.0	2763	4	US-08-921-954-14	Sequence 14, Appl
	8	190	100.0	2763	5	PCT-US94-14919-1	Sequence 1, Appli
	9	190	100.0	2763	5	PCT-US94-14920-1	Sequence 1, Appli
	10	190	100.0	3083	3	US-08-956-657-1	Sequence 1, Appli
	11	190	100.0	3083	4	US-09-335-231-25	Sequence 25, Appl
	12	86.8	45.7	1104	4	US-09-270-767-13253	Sequence 13253, A
	13	54.6	28.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	14	54.6	28.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	15	39.8	20.9	738	4	US-09-248-796A-3979	Sequence 3979, Ap
	16	34.8	18.3	849	4	US-09-134-000C-2607	Sequence 2607, Ap
c	17	31.8	16.7	486	2	US-08-199-984-7	Sequence 7, Appli
c	18	30	15.8	2119	4	US-09-620-312D-35	Sequence 35, Appl
	19	29.6	15.6	1542	4	US-09-489-039A-5706	Sequence 5706, Ap
	20	28.8	15.2	465	4	US-09-489-039A-1090	Sequence 1090, Ap
c	21	28.8	15.2	1278	4	US-09-489-039A-1038	Sequence 1038, Ap
	22	28.4	14.9	600	4	US-09-248-796A-3980	Sequence 3980, Ap
	23	28.4	14.9	987	4	US-09-252-991A-10424	Sequence 10424, A
	24	28.4	14.9	1350	4	US-09-270-767-10435	Sequence 10435, A
	25	28.4	14.9	1422	4	US-09-252-991A-10517	Sequence 10517, A
c	26	28.4	14.9	2133	4	US-09-252-991A-10738	Sequence 10738, A
c	27	28.4	14.9	48974	3	US-08-920-422-17	Sequence 17, Appl
	28	28	14.7	160	2	US-08-890-980-26	Sequence 26, Appl
	29	28	14.7	160	3	US-08-890-979-26	Sequence 26, Appl
	30	28	14.7	160	3	US-09-032-894-26	Sequence 26, Appl
	31	28	14.7	160	3	US-09-031-626-26	Sequence 26, Appl
	32	28	14.7	416	2	US-08-890-980-9	Sequence 9, Appli
	33	28	14.7	416	3	US-08-890-979-9	Sequence 9, Appli
	34	28	14.7	416	3	US-09-032-894-9	Sequence 9, Appli
	35	28	14.7	416	3	US-09-031-626-9	Sequence 9, Appli
	36	27.8	14.6	570	4	US-09-134-000C-33	Sequence 33, Appl
	37	27.8	14.6	876	4	US-09-107-532A-1498	Sequence 1498, Ap
	38	27.6	14.5	957	4	US-09-489-039A-3296	Sequence 3296, Ap
c	39	27.6	14.5	1260	4	US-09-489-039A-3298	Sequence 3298, Ap
	40	27.4	14.4	12848	3	US-09-453-702B-252	Sequence 252, App
c	41	27.4	14.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	42	27.4	14.4	1664976	4	US-09-692-570-1	Sequence 1, Appli
	43	27.2	14.3	3058	3	US-08-818-112-106	Sequence 106, App
	44	27.2	14.3	3058	3	US-08-818-111-101	Sequence 101, App
	45	27.2	14.3	3058	3	US-09-056-556-106	Sequence 106, App

ALIGNMENTS

```
RESULT 1
US-08-921-954-23
; Sequence 23, Application US/08921954
; Patent No. 6689864
;  GENERAL INFORMATION:
;       APPLICANT: Carson, Dennis A.
;                  No. 6689864ori, Tsutomu
;       TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
;                           Detection of Cancer, Monitoring of Tumor Progression and
;                           Cancer Treatment
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/921,954
;            FILING DATE: 26-Aug-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/908,671A
;            FILING DATE: 18-Jul-2001
;            APPLICATION NUMBER: US 08/921,954
;            FILING DATE: 20-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hinsch, Matthew E.
;            REGISTRATION NUMBER: 47,651
;            REFERENCE/DOCKET NUMBER: 023070-104042US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1450 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..1450
;            OTHER INFORMATION:  /note= "methylthioadenosine
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```
;             phosphorylase (MTAse) genomic nucleotide
;             sequence"
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  254..421
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  616..720
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  964..1203
;         SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-921-954-23

  Query Match             100.0%;  Score 190;  DB 4;  Length 1450;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5571510ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    TITLE OF INVENTION:  METHOD FOR SELECTIVE METHIONINE
;    TITLE OF INVENTION:  STARVATION OF MALIGNANT CELLS IN MAMMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,413
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD2864
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-176-413-1

  Query Match             100.0%;  Score 190;  DB 1;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 3
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
;  GENERAL INFORMATION:
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    APPLICANT:  No. 5840505ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    TITLE OF INVENTION:  METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
;    TITLE OF INVENTION:  ACTIVITY IN MALIGNANT METHYLTHIOADENOSINE PHOSPHORYLASE DEFICI
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,542B
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 678-5070
;      TELEFAX:  (619) 678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
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;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-612-542B-1

  Query Match             100.0%;  Score 190;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 4
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5942393ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Takabayashi, Kenji
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/772,113
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,855
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
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;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-772-113-1

  Query Match             100.0%;  Score 190;  DB 2;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 5
US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6214571ori, Tsutomu
;    APPLICANT:  Carson, Dennis A.
;    APPLICANT:  Carrera, Carlos J.
;    APPLICANT:  Cottam, Howard B.
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,137
;      FILING DATE:  24-NOV-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howells, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  PD3057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
```

```
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-09-199-137-1

  Query Match             100.0%;  Score 190;  DB 3;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 6
US-08-227-800A-14
; Sequence 14, Application US/08227800A
; Patent No. 6689561
;  GENERAL INFORMATION:
;    APPLICANT:  CARSON, DENNIS A.
;    APPLICANT:  NOBORI, TSUTOMU
;    TITLE OF INVENTION:  TUMOR SUPPRESSOR GENE AND METHODS FOR
;    TITLE OF INVENTION:  DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANCE
;    TITLE OF INVENTION:  TREATMENT
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/227,800A
;      FILING DATE:  14-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOWELLS, STACY L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/023001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Methylthioadenosine Phosphorylase (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
US-08-227-800A-14

  Query Match             100.0%;  Score 190;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 7
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
;   GENERAL INFORMATION:
;        APPLICANT: Carson, Dennis A.
;                   No. 6689864ori, Tsutomu
;        TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
;                            Detection of Cancer, Monitoring of Tumor Progression and
;                            Cancer Treatment
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/921,954
;             FILING DATE: 26-Aug-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671A
;             FILING DATE: 18-Jul-2001
;             APPLICATION NUMBER: US 08/921,954
;             FILING DATE: 20-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hinsch, Matthew E.
;             REGISTRATION NUMBER: 47,651
;             REFERENCE/DOCKET NUMBER: 023070-104042US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  1..2763
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;             OTHER INFORMATION:  /note= "full-length
;             methylthioadenosine phosphorylase
;             (MTAse) genomic nucleotide sequence"
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  254..421
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  616..720
;         FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  964..1203
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

  Query Match             100.0%;  Score 190;  DB 4;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 8
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR SELECTIVE METHIONINE
;    TITLE OF INVENTION:  STARVATION OF MALIGNANT CELLS IN MAMMALS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14919
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-286
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14919-1

  Query Match             100.0%;  Score 190;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 9
PCT-US94-14920-1
; Sequence 1, Application PC/TUS9414920
;  GENERAL INFORMATION:
;    APPLICANT:  THE REGENTS OF THE UNIVERSITY
;    APPLICANT:  OF CALIFORNIA
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14920
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-287
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-977-1001
;      TELEFAX:  213-977-1003
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2763 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  methyladenosine phosphatase
;    FEATURE:
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;      NAME/KEY:  CDS
;      LOCATION:  1..2763
PCT-US94-14920-1

  Query Match             100.0%;  Score 190;  DB 5;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 10
US-08-956-657-1
; Sequence 1, Application US/08956657
; Patent No. 6210917
;  GENERAL INFORMATION:
;    APPLICANT:  No. 6210917ori et al., Tsutomu
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF
;    TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/956,657
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/827,342
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,855
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Taylor, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07340/050001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3083 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-956-657-1

  Query Match             100.0%;  Score 190;  DB 3;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 11
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE:  023070-108010US
;  CURRENT APPLICATION NUMBER: US/09/335,231
;  CURRENT FILING DATE:  1999-06-17
;  PRIOR APPLICATION NUMBER:  US 60/090,411
;  PRIOR FILING DATE:  1998-06-23
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-09-335-231-25
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  Query Match             100.0%;  Score 190;  DB 4;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 12
US-09-270-767-13253
; Sequence 13253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13253
;   LENGTH: 1104
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-13253

  Query Match             45.7%;  Score 86.8;  DB 4;  Length 1104;
  Best Local Similarity   66.7%;  Pred. No. 4.6e-22;
  Matches  124;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy          2 TTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTCA 61
              ||||  |  || | || ||| |||| |   | |    ||||   ||||  || || || |
Db        538 TTCTGCTTCAGGCGGCCAAGGAGCTGGAGATTCCCGCCCACGATAAGGCCACCATTGTGA 597

Qy         62 CAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGGG 121
              | || ||||| || || ||   ||| ||  | || |||  |||||||||    ||||| |
Db        598 CTATTGAGGGTCCGCGCTTCTCCTCTCGCTCGGAGAGCCACATGTTCCGTCAGTGGGGCG 657

Qy        122 CGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATTT 181
              |||  | || ||||||||||   |||||| ||||| || || ||||||||||  |
Db        658 GGGACCTCATAAACATGACCACGTGTCCAGAAGTGGTGCTAGCCAAGGAGGCTGGCCTAC 717

Qy        182 GTTACG 187
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Db        718 TTTACG 723


RESULT 13
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             28.7%;  Score 54.6;  DB 3;  Length 4403765;
  Best Local Similarity   61.7%;  Pred. No. 1.7e-08;
  Matches   87;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         49 GGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTC 108
              || || |||||    ||| |||| || || |||  | |||| || ||||||      ||||
Db     628349 GGCACCATGGTGGTGATCCAGGGTCCGCGGTTTTCCACCCGCGCGGAAAGCCAGTGGTTC 628408

Qy        109 CGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAG 168
               | |    |||    || |  ||||||||||      ||| |||| ||| || |||
Db     628409 GCCGCTGCCGGGTGCAATCTGGTCAACATGACCGGCTATCCCGAGGCGGTGCTGGCTCGC 628468

Qy        169 GAGGCTGGAATTTGTTACGCA 189
              ||    | | | || ||||||
Db     628469 GAACTCGAATTATGCTACGCA 628489


RESULT 14
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             28.7%;  Score 54.6;  DB 3;  Length 4411529;
  Best Local Similarity   61.7%;  Pred. No. 1.7e-08;
  Matches   87;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         49 GGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTC 108
              || || |||||    ||| |||| || || |||  | |||| || ||||||      ||||
Db     626905 GGCACCATGGTGGTGATCCAGGGTCCGCGGTTTTCCACCCGCGCGGAAAGCCAGTGGTTC 626964

Qy        109 CGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAG 168
               | |    |||    || |  ||||||||||      ||| |||| ||| || |||
Db     626965 GCCGCTGCCGGGTGCAATCTGGTCAACATGACCGGCTATCCCGAGGCGGTGCTGGCTCGC 627024

Qy        169 GAGGCTGGAATTTGTTACGCA 189
              ||    | | | || ||||||
Db     627025 GAACTCGAATTATGCTACGCA 627045


RESULT 15
US-09-248-796A-3979
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; Sequence 3979, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3979
;   LENGTH: 738
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-3979

  Query Match             20.9%;  Score 39.8;  DB 4;  Length 738;
  Best Local Similarity   55.4%;  Pred. No. 9.1e-05;
  Matches   77;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy          52 ACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGC 111
               || ||  ||   || ||||| || |  |||    || | || |||        | | | |
Db         331 ACCATCATCTGTATGGAGGGCCCGCAGTTTTCAACCAGAGCTGAATCTAGATTATACAGA 390

Qy         112 ACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAG 171
               | |||||| |    ||| || || ||| |   | | ||||| |       | |||   ||
Db         391 AGCTGGGGAGGTTCTGTCATTAATATGTCAGTATTGCCAGAAGCCAAATTAGCTCGTGAA 450

Qy         172 GCTGGAATTTGTTACGCAA 190
               || | ||||  ||||  ||
Db         451 GCAGAAATTGCTTACCAAA 469


Search completed: February  1, 2005, 15:01:17
Job time : 67.497 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	190	100.0	870	16	US-10-367-366-1	Sequence 1, Appli
	2	190	100.0	2269	18	US-10-779-476-2	Sequence 2, Appli
	3	190	100.0	2763	10	US-09-908-671-14	Sequence 14, Appl
	4	190	100.0	3083	9	US-09-780-114-1	Sequence 1, Appli
	5	190	100.0	3083	15	US-10-326-681-25	Sequence 25, Appl
	6	135.2	71.2	662	11	US-09-969-034-2820	Sequence 2820, Ap
	7	119	62.6	441	9	US-09-867-701-4027	Sequence 4027, Ap
	8	53.2	28.0	1029	18	US-10-653-047-7072	Sequence 7072, Ap
c	9	50.2	26.4	661	18	US-10-425-115-101607	Sequence 101607,
	10	40	21.1	390	9	US-09-960-352-6576	Sequence 6576, Ap
	11	35.2	18.5	870	18	US-10-873-595-53	Sequence 53, Appl
	12	35.2	18.5	1418	9	US-09-782-378A-21	Sequence 21, Appl
	13	35.2	18.5	1418	15	US-10-021-660-17	Sequence 17, Appl
	14	35.2	18.5	1418	15	US-10-354-358-61	Sequence 61, Appl
	15	35.2	18.5	1418	15	US-10-172-118-458	Sequence 458, App
	16	35.2	18.5	1418	16	US-10-211-462-142	Sequence 142, App
	17	35.2	18.5	1418	16	US-10-342-887-458	Sequence 458, App
	18	35.2	18.5	1418	17	US-10-717-597-123	Sequence 123, App
	19	35.2	18.5	1492	15	US-10-133-013-267	Sequence 267, App
c	20	34.8	18.3	16484	9	US-09-070-927A-158	Sequence 158, App
	21	34.8	18.3	319630	16	US-10-398-221-7	Sequence 7, Appli
c	22	34.8	18.3	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
c	23	33.2	17.5	471	16	US-10-242-535A-40954	Sequence 40954, A
c	24	33.2	17.5	471	16	US-10-085-783A-40954	Sequence 40954, A
c	25	33.2	17.5	1434	16	US-10-398-221-3336	Sequence 3336, Ap
	26	32.8	17.3	831	15	US-10-156-761-3666	Sequence 3666, Ap
	27	32.8	17.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	28	31.2	16.4	507	9	US-09-878-178-1002	Sequence 1002, Ap
c	29	31.2	16.4	507	13	US-10-046-935-1002	Sequence 1002, Ap
c	30	31.2	16.4	507	14	US-10-146-502-1002	Sequence 1002, Ap
	31	30.6	16.1	255	16	US-10-424-599-109850	Sequence 109850,
	32	30.6	16.1	813	18	US-10-425-115-33898	Sequence 33898, A
c	33	30.2	15.9	561515	17	US-10-741-601-5682	Sequence 5682, Ap
	34	30	15.8	293	17	US-10-437-963-20596	Sequence 20596, A
c	35	30	15.8	1257	16	US-10-343-650A-49	Sequence 49, Appl
c	36	30	15.8	1338	15	US-10-275-554-1	Sequence 1, Appli
c	37	30	15.8	1732	15	US-10-029-656-11	Sequence 11, Appl
	38	30	15.8	1741	9	US-09-823-245A-350	Sequence 350, App
c	39	30	15.8	1853	15	US-10-029-656-9	Sequence 9, Appli
c	40	30	15.8	1892	16	US-10-264-237-1324	Sequence 1324, Ap
c	41	30	15.8	2119	15	US-10-037-270-35	Sequence 35, Appl
c	42	30	15.8	2119	15	US-10-117-722-35	Sequence 35, Appl
c	43	30	15.8	2171	15	US-10-241-220-47	Sequence 47, Appl
c	44	30	15.8	2171	18	US-10-872-972-47	Sequence 47, Appl
c	45	30	15.8	2171	18	US-10-872-991-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Pei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skalitzky , Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; TITLE OF INVENTION: Phosphorylase Deficient Cells
; FILE REFERENCE: PC19080A (AG110-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

Query Match 100.0%; Score 190; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 7.1e-61;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db        457 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 516

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
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Db        517 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 576

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
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Db        577 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 636

Qy        181 TGTTACGCAA 190
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Db        637 TGTTACGCAA 646


RESULT 2
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
;  APPLICANT: Salmedix, Inc.
;  APPLICANT:  Leoni,Lorenzo M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
;  TITLE OF INVENTION:  METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
;  FILE REFERENCE: 076936-0307942
;  CURRENT APPLICATION NUMBER: US/10/779,476
;  CURRENT FILING DATE:  2004-02-13
;  PRIOR APPLICATION NUMBER: 60/447,888
;  PRIOR FILING DATE: 2003-02-14
;  PRIOR APPLICATION NUMBER: 60/460,715
;  PRIOR FILING DATE: 2004-04-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 2269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-779-476-2

  Query Match            100.0%;  Score 190;  DB 18;  Length 2269;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-61;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 631

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 691

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 751

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        752 TGTTACGCAA 761


RESULT 3
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
;   GENERAL INFORMATION:
;        APPLICANT: CARSON, DENNIS A.
;                   NOBORI, TSUTOMU
;        TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
;                            DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
;                            TREATMENT
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: California
;             COUNTRY: US
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/908,671
;             FILING DATE: 18-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/227,800
;             FILING DATE: 14-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HOWELLS, STACY L.
;             REGISTRATION NUMBER: 34,842
;             REFERENCE/DOCKET NUMBER: 07340/023001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
;             TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2763 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        IMMEDIATE SOURCE:
;             CLONE: Methylthioadenosine Phosphorylase (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..2763
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

  Query Match            100.0%;  Score 190;  DB 10;  Length 2763;
  Best Local Similarity   100.0%;  Pred. No. 1e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1023

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1083

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1143

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1144 TGTTACGCAA 1153


RESULT 4
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
;   GENERAL INFORMATION:
;        APPLICANT: No. US20020146695A1ori, Tsutomu
;                   Carson, Dennis A.
;                   Takabayashi, Kenji
;        TITLE OF INVENTION: Method for Detection of the Presence or
;                            Absence of Methylthioadenosine Phosphorylase
;                            (MTAse) in a
;                            Cell Sample by Detection of the Presence or Absence
;        NUMBER OF SEQUENCES: 1
```

```
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/780,114
;            FILING DATE: 09-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/072,914
;            FILING DATE: 04-May-1998
;            APPLICATION NUMBER: US 08/176,855
;            FILING DATE: 29-DEC-1993
;            APPLICATION NUMBER: US 08/459,343
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 08/827,342
;            FILING DATE: 26-MAR-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bastian, Kevin L.
;            REGISTRATION NUMBER: 34,774
;            REFERENCE/DOCKET NUMBER: 023070-103030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3083 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..3083
;            OTHER INFORMATION:  /note= "rat methylthioadenosine
;            phosphorylase (MTAse)"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  119..151
;            OTHER INFORMATION:  /note= "exon 1"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  450..536
;            OTHER INFORMATION:  /note= "exon 2"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  724..782
;            OTHER INFORMATION:  /note= "exon 3"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  899..1066
;            OTHER INFORMATION:  /note= "exon 4"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1378..1480
;            OTHER INFORMATION:  /note= "exon 5"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  1764..1953
;            OTHER INFORMATION:  /note= "exon 6"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2426..2548
;            OTHER INFORMATION:  /note= "exon 7"
;       FEATURE:
;            NAME/KEY:  exon
;            LOCATION:  2838..2876
;            OTHER INFORMATION:  /note= "exon 8"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

  Query Match             100.0%;  Score 190;  DB 9;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 5
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;  APPLICANT: Carson, Dennis A.
;  APPLICANT:  Schmid, Mathias
;  APPLICANT:  Carrera, Carlos J.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
;  TITLE OF INVENTION:  Prognosis in, Cancer
;  FILE REFERENCE: 023070-108010US
;  CURRENT APPLICATION NUMBER: US/10/326,681
;  CURRENT FILING DATE:  2003-04-15
;  PRIOR APPLICATION NUMBER: US 60/090,411
;  PRIOR FILING DATE: 1998-06-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
;   FEATURE:
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;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-10-326-681-25

  Query Match             100.0%;  Score 190;  DB 15;  Length 3083;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-60;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 1823

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 1883

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 1943

Qy        181 TGTTACGCAA 190
              ||||||||||
Db       1944 TGTTACGCAA 1953


RESULT 6
US-09-969-034-2820
; Sequence 2820, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT:  Astle, Jon H.
;  APPLICANT:  Carroll, Eddie III
;  APPLICANT:  Catino, Theodore J.
;  APPLICANT:  Dwivedi, Poornima
;  APPLICANT:  Molino, Gary A.
;  APPLICANT:  Thiagalingam, Arunthathi
;  APPLICANT:  Lewis, Marcia E.
;  TITLE OF INVENTION: Nucleic Acid Sequences Differentially
;  TITLE OF INVENTION:  Expressed in Cancer Tissue
;  FILE REFERENCE: 1657/1032
;  CURRENT APPLICATION NUMBER: US/09/969,034
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: 60/237,271
;  PRIOR FILING DATE: 2000-02-10
;  NUMBER OF SEQ ID NOS: 4494
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2820
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 51, 127, 216, 234, 235, 240, 289, 315, 338, 362, 365, 390,
;   LOCATION: 402, 405, 410, 411, 432, 436, 442, 460, 466, 487, 493, 506,
;   LOCATION: 509, 512, 525, 526, 537, 551, 560, 566, 570, 576, 581, 583,
;   LOCATION: 588, 609, 611, 621, 632, 636, 649, 657
;   OTHER INFORMATION: n = A,T,C or G
US-09-969-034-2820

  Query Match             71.2%;  Score 135.2;  DB 11;  Length 662;
  Best Local Similarity   90.1%;  Pred. No. 3e-40;
  Matches  173;  Conservative    0;  Mismatches   16;  Indels    3;  Gaps    3;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              |||||||||||||||||||||| ||||||||||||||||  |||| ||||||||||||||
Db        194 GTTCTTATAGAGACTGCTAAGANGCTAGGACTCCGGTGCCNNTCAANGGGGACAATGGTC 253

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              |||||||||||||||| |||||||||||    || ||||||||||||||||||||||||
Db        254 ACAATCGAGGGACCTCG-TTTAGCTCCCGGCAGAAANGCTTCATGTTCCGCACCTGGGGG 312

Qy        121 GC-GGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCT-AAGGAGGCTGGAA 178
              || |||||||||||||||||| || ||||||||| | ||||| || || |||||||
Db        313 GCNGGATGTTATCAACATGACCACANTTTCAGAGGTGGGTTTTGCTAAANGANGCTGGAA 372

Qy        179 TTTGTTACGCAA 190
              |||| |||||||
Db        373 TTTGATACGCAA 384


RESULT 7
US-09-867-701-4027
; Sequence 4027, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Aglate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4027
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(441)
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-4027

  Query Match             62.6%;  Score 119;  DB 9;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-34;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 382

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 441


RESULT 8
US-10-653-047-7072
; Sequence 7072, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
;  APPLICANT: Randy M. Berka
;  APPLICANT:  Michael W. Rey
;  APPLICANT:  Jeffrey R.Shuster
;  APPLICANT:  Sakari Kauppinen
;  APPLICANT:  Ib Groth Clausen
;  APPLICANT:  Peter Bjarke Olsen
;  TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE: 5849.200-US
```

```
;  CURRENT APPLICATION NUMBER: US/10/653,047
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/533,559
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/273,623
;  PRIOR FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 7860
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7072
;   LENGTH: 1029
;   TYPE: DNA
;   ORGANISM: Aspergillus oryzae
US-10-653-047-7072

  Query Match             28.0%;  Score 53.2;  DB 18;  Length 1029;
  Best Local Similarity   61.6%;  Pred. No. 2.9e-09;
  Matches   85;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         49 GGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTC 108
              || ||| ||||    || ||||||||||  ||   | | || || || ||      | | |
Db        581 GGCACATTGGTGTGCATGGAGGGACCTCAATTCTCCACTCGCGCCGAGAGTAAGCTCTAC 640

Qy        109 CGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAG 168
              ||| ||||||| |      || |||||||| |      |||| |||| |    || |||
Db        641 CGCTCCTGGGGTGGCAGCGTCATCAACATGTCTTGTCTTCCTGAGGCGAAGCTGGCTCGT 700

Qy        169 GAGGCTGGAATTTGTTAC 186
              ||||| |  |||   |||
Db        701 GAGGCCGAGATTGCCTAC 718


RESULT 9
US-10-425-115-101607/c
; Sequence 101607, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 101607
;   LENGTH: 661
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_24177C.1
US-10-425-115-101607

  Query Match             26.4%;  Score 50.2;  DB 18;  Length 661;
  Best Local Similarity   62.2%;  Pred. No. 3.4e-08;
  Matches   79;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy         64 ATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGGGCG 123
              || ||||| || |  ||     |||| || || |||  | | | ||| | ||||||    |
Db        309 ATGGAGGGGCCGCAGTTCTCGACCCGCGCCGAGAGCAACCTCTACCGGAGCTGGGGCATG 250

Qy        124 GATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATTTGT 183
              || || |||  |||||||   | || ||||     || ||    |||| |  || ||
Db        249 GACGTCATCGGCATGACCAACATGCCGGAGGCCAAGCTCGCGCGCGAGGCCGAGATCTGC 190

Qy        184 TACGCAA 190
              ||||| |
Db        189 TACGCGA 183


RESULT 10
US-09-960-352-6576
; Sequence 6576, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6576
;   LENGTH: 390
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 28-LIB34-028-Q1-E1-G7
US-09-960-352-6576

  Query Match             21.1%;  Score 40;  DB 9;  Length 390;
  Best Local Similarity   55.9%;  Pred. No. 0.0002;
  Matches   76;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy         47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
              | || ||    || |  | | ||| ||   ||||    |  ||||| |   | ||
Db         36 AAGGCACCTACGTGATGTTGGGGGGTCCCAATTTTGAGACTGTGGCAGAGTGTCGCCTGC 95

Qy        107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
              | || |     ||||| |||| | |   ||||| |||||| ||||| ||  |  | || |
Db         96 TGCGGAATCTAGGGGCAGATGCTGTTGGCATGAGCACAGTACCAGAAGTTATAGTCGCAA 155

Qy        167 AGGAGGCTGGAATTTG 182
              |   |||| || |
Db        156 GACACTGTGGACTTCG 171


RESULT 11
US-10-873-595-53
; Sequence 53, Application US/10873595
; Publication No. US20040265889A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF BIOMARKERS FOR LIVER TOXICITY
;  FILE REFERENCE: D0325 NP
;  CURRENT APPLICATION NUMBER: US/10/873,595
;  CURRENT FILING DATE:  2004-06-22
;  PRIOR APPLICATION NUMBER: U.S. 60/480,964
;  PRIOR FILING DATE: 2003-06-24
;  PRIOR APPLICATION NUMBER: U.S. 60/529,806
;  PRIOR FILING DATE: 2003-12-16
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
;   LENGTH: 870
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-873-595-53

  Query Match             18.5%;  Score 35.2;  DB 18;  Length 870;
  Best Local Similarity   53.7%;  Pred. No. 0.017;
  Matches   73;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy         47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
              | || ||    || |  | | || ||  | |||     |  |||||| |     ||
Db        566 AAGGCACCTATGTGATGGTGGCAGGCCCCAGCTTTGAGACTGTGGCAGAATGTCGTGTGC 625

Qy        107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
              | |  |    ||| || || | | |   |||||  ||||| ||||| ||  |  ||||
Db        626 TGCAGAAGCTGGGAGCAGACGCTGTTGGCATGAGTACAGTACCAGAAGTTATCGTTGCAC 685

Qy        167 AGGAGGCTGGAATTTG 182
              | |   |||| || |
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Db        686 GGCACTGTGGACTTCG 701


RESULT 12
US-09-782-378A-21
; Sequence 21, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
;  APPLICANT: Hearing, Patrick
;  APPLICANT:  Bahou, Wadie
;  APPLICANT:  Sandalon, Ziv
;  APPLICANT:  Gnatenko, Dmitri
;  TITLE OF INVENTION: Adenoviral Vectors
;  FILE REFERENCE: STONYB-04970
;  CURRENT APPLICATION NUMBER: US/09/782,378A
;  CURRENT FILING DATE:  2001-02-12
;  PRIOR APPLICATION NUMBER: 60/237,747
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 1418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-782-378A-21

  Query Match             18.5%;  Score 35.2;  DB 9;  Length 1418;
  Best Local Similarity   53.7%;  Pred. No. 0.02;
  Matches   73;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy         47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
              | || ||    || |  | |  || ||  | |||    |   ||||||| |     ||
Db        675 AAGGCACCTATGTGATGGTGGCAGGCCCCAGCTTTGAGACTGTGGCAGAATGTCGTGTGC 734

Qy        107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
              | |  |    ||| || || | | |   |||||  ||||| ||||| ||  |  ||||
Db        735 TGCAGAAGCTGGGAGCAGACGCTGTTGGCATGAGTACAGTACCAGAAGTTATCGTTGCAC 794

Qy        167 AGGAGGCTGGAATTTG 182
                | |   |||| || |
Db        795 GGCACTGTGGACTTCG 810


RESULT 13
US-10-021-660-17
; Sequence 17, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
;  APPLICANT: Murray, Richard
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  EOS Biotechnology, Inc.
;  TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
;  TITLE OF INVENTION:  Compositions and Methods of Screening for Angiogenesis
;  TITLE OF INVENTION:  Modulators
;  FILE REFERENCE: 018501-000710US
;  CURRENT APPLICATION NUMBER: US/10/021,660
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: US/09/784,356
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: US 09/637,977
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 1418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-021-660-17

  Query Match             18.5%;  Score 35.2;  DB 15;  Length 1418;
  Best Local Similarity   53.7%;  Pred. No. 0.02;
  Matches   73;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy         47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
              | || ||    || |  | |  || ||  | |||    |   ||||||| |     ||
Db        675 AAGGCACCTATGTGATGGTGGCAGGCCCCAGCTTTGAGACTGTGGCAGAATGTCGTGTGC 734

Qy        107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
              | |  |    ||| || || | | |   |||||  ||||| ||||| ||  |  ||||
Db        735 TGCAGAAGCTGGGAGCAGACGCTGTTGGCATGAGTACAGTACCAGAAGTTATCGTTGCAC 794

Qy        167 AGGAGGCTGGAATTTG 182
                | |   |||| || |
Db        795 GGCACTGTGGACTTCG 810


RESULT 14
US-10-354-358-61
; Sequence 61, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Hunter, John Joseph
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Tsai, Fong-Ying
;  APPLICANT:  Lesoon, Andrea
;  APPLICANT:  Lightcap, Eric S.
;  APPLICANT:  Williamson, Mark
;  APPLICANT:  Rudolph-Owen, Laura A.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
;  TITLE OF INVENTION:  7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
;  TITLE OF INVENTION:  3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
;  TITLE OF INVENTION:  9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
;  TITLE OF INVENTION:  8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
;  TITLE OF INVENTION:  16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
;  TITLE OF INVENTION:  2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
;  FILE REFERENCE: MPI02-020P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/354,358
;  CURRENT FILING DATE:  2003-01-30
;  PRIOR APPLICATION NUMBER: US 60/353,600
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: US 60/364,517
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/371,075
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/371,507
;  PRIOR FILING DATE: 2002-04-10
;  PRIOR APPLICATION NUMBER: US 60/372,984
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: US 60/374,194
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/382,995
;  PRIOR FILING DATE: 2002-05-24
;  PRIOR APPLICATION NUMBER: US 60/385,023
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/388,853
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/389,395
;  PRIOR FILING DATE: 2002-06-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 1418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (110)...(979)
US-10-354-358-61

  Query Match             18.5%;  Score 35.2;  DB 15;  Length 1418;
  Best Local Similarity   53.7%;  Pred. No. 0.02;
  Matches   73;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;
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Qy          47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
               | || ||    || |   | |  || ||  | |||    |   ||||||| |     ||
Db         675 AAGGCACCTATGTGATGGTGGCAGGCCCCAGCTTTGAGACTGTGGCAGAATGTCGTGTGC 734

Qy         107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
               | |  |    ||| || || | | |   |||||  ||||| ||||| ||  |  ||||
Db         735 TGCAGAAGCTGGGAGCAGACGCTGTTGGCATGAGTACAGTACCAGAAGTTATCGTTGCAC 794

Qy         167 AGGAGGCTGGAATTTG 182
               | |   |||| || |
Db         795 GGCACTGTGGACTTCG 810
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RESULT 15
US-10-172-118-458
; Sequence 458, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 458
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000270
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-458

Query Match 18.5%; Score 35.2; DB 15; Length 1418;
Best Local Similarity 53.7%; Pred. No. 0.02;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Qy          47 AGGGGACAATGGTCACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGT 106
               | || ||    || |   | |  || ||  | |||    |   ||||||| |     ||
Db         675 AAGGCACCTATGTGATGGTGGCAGGCCCCAGCTTTGAGACTGTGGCAGAATGTCGTGTGC 734

Qy         107 TCCGCACCTGGGGGGCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTA 166
               | |  |    ||| || || | | |   |||||  ||||| ||||| ||  |  ||||
Db         735 TGCAGAAGCTGGGAGCAGACGCTGTTGGCATGAGTACAGTACCAGAAGTTATCGTTGCAC 794

Qy         167 AGGAGGCTGGAATTTG 182
               | |   |||| || |
Db         795 GGCACTGTGGACTTCG 810
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Search completed: February 1, 2005, 17:20:50
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 2136.25 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGGAATTTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	190	100.0	509	7	CN409509	CN409509 170004239
2	190	100.0	562	7	CN409511	CN409511 170006000
3	190	100.0	580	4	BM839857	BM839857 K-EST0116
4	190	100.0	580	4	BM840883	BM840883 K-EST0118
5	190	100.0	638	7	CN409513	CN409513 170005327
6	190	100.0	738	2	BF792159	BF792159 602252620
7	190	100.0	751	7	CN409512	CN409512 170005829
8	190	100.0	813	9	AY405891	AY405891 Homo sapi
9	190	100.0	1037	4	BM903599	BM903599 AGENCOURT
10	190	100.0	1047	4	BM925551	BM925551 AGENCOURT
11	190	100.0	1064	5	BX459089	BX459089 BX459089
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13	190	100.0	1380	3	BC012316	BC012316 Homo sapi
14	189	99.5	910	4	BM459757	BM459757 AGENCOURT
15	188.4	99.2	728	4	BG501032	BG501032 602546438
16	188.4	99.2	745	7	CN409510	CN409510 170005999
17	188.4	99.2	774	7	CN409507	CN409507 170006000
18	188.4	99.2	880	5	BX374546	BX374546 BX374546
19	188.4	99.2	885	5	BX374675	BX374675 BX374675
20	186.8	98.3	838	4	BM014199	BM014199 603639894
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22	185	97.4	813	9	AY405892	AY405892 Pan trogl
23	183.6	96.6	764	4	BM423110	BM423110 PLATE1_G0
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26	172.4	90.7	950	7	CF413058	CF413058 CH3#083_G
27	170.4	89.7	732	6	CD643696	CD643696 AGENCOURT
28	169.8	89.4	766	7	CO738989	CO738989 S1LE04c22
29	168.2	88.5	771	7	CO737569	CO737569 S1LH03c18
30	168	88.4	751	7	CN409514	CN409514 170005322
31	167.6	88.2	484	7	CF930825	CF930825 CF--05-R-
32	167.6	88.2	562	4	BI774611	BI774611 466793 MA
33	167.6	88.2	682	7	CN788377	CN788377 4122709 B
34	167.6	88.2	692	7	CK968775	CK968775 4084058 B
c 35	164.4	86.5	679	2	AW150875	AW150875 xg41d10.x
36	159.6	84.0	756	4	BG704891	BG704891 602688547
37	157.2	82.7	448	2	AW430599	AW430599 70314 MAR
38	154.8	81.5	400	1	AA221942	AA221942 mw16a04.r
39	154.8	81.5	414	7	CK391396	CK391396 K0831A05-
40	154.8	81.5	488	1	AA939482	AA939482 vz50b06.r
41	154.8	81.5	555	6	CD544714	CD544714 B0260B09-
42	154.8	81.5	620	7	CK621557	CK621557 ml25g11.y
43	154.8	81.5	637	6	CD806610	CD806610 UI-M-GW0-
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45	154.8	81.5	764	6	CB237920	CB237920 AGENCOURT

ALIGNMENTS

RESULT 1
CN409509
LOCUS CN409509 509 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000423957987 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409509
VERSION CN409509.1 GI:47396633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 509 Std Error: 0.00.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
ORIGIN

Query Match 100.0%; Score 190; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db        181 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 240
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Qy          61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 300

Qy         121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 360

Qy         181 TGTTACGCAA 190
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Db         361 TGTTACGCAA 370


RESULT 2
CN409511
LOCUS       CN409511                562 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000600010132 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN409511
VERSION     CN409511.1  GI:47396635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 562   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .562
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     line"
                     /clone_lib="GRN_PREHEP"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from DMSO-treated hES cell line H9 (p22) maintained in
                     feeder-free conditions"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 7;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 241

Qy          61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 301

Qy         121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 361

Qy         181 TGTTACGCAA 190
               ||||||||||
Db         362 TGTTACGCAA 371


RESULT 3
BM839857
LOCUS       BM839857                580 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0116831 S13KMS5 Homo sapiens cDNA clone S13KMS5-31-A07 5',
            mRNA sequence.
ACCESSION   BM839857
VERSION     BM839857.1  GI:19196266
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 31  row: A  column: 07
            High quality sequence stop: 580.
FEATURES             Location/Qualifiers
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                     /clone="S13KMS5-31-A07"
                     /tissue_type="myeloma"
                     /cell_line="KMS-5"
                     /lab_host="Top10F'"
                     /clone_lib="S13KMS5"
                     /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
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                     phosphatase (BAP) and then decapped with tabacco acid
                     pyrophosphatase (TAP). The decapped intact mRNA was
                     ligated with DNA-RNA linker including EcoR I site by
                     treatment of T4 RNA ligase and the first strand cDNA was
                     synthesized from oligo dT-selected mRNA by priming with
                     dT-tailed vector. The dT-tailed vector was adjusted to
                     have about 60nt. The cDNA vector was circularized with E.
                     coli DNA ligase after digestion of EcoRI which site is
                     also included in vector. An RNA strand converted to a DNA
                     strand by Okayama-Berg method. The obtained cDNA vectors
                     were used for transformation of competent cells E. coli
                     Top10F' by electroporation method. The cDNA libraries
                     constructed by this method are full-length enriched cDNA
                     library."
ORIGIN

  Query Match             100.0%;  Score 190;  DB 4;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 279

Qy          61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 339

Qy         121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 399

Qy         181 TGTTACGCAA 190
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              ||||||||||
Db        400 TGTTACGCAA 409


RESULT 4
BM840883
LOCUS       BM840883                 580 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0118036 S13KMS5 Homo sapiens cDNA clone S13KMS5-35-F08 5',
            mRNA sequence.
ACCESSION   BM840883
VERSION     BM840883.1  GI:19197292
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 35  row: F  column: 08
            High quality sequence stop: 580.
FEATURES             Location/Qualifiers
     source          1. .580
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S13KMS5-35-F08"
                     /tissue_type="myeloma"
                     /cell_line="KMS-5"
                     /lab_host="Top10F'"
                     /clone_lib="S13KMS5"
                     /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
                     (A)+ RNA was dephosphorylated with bacterial alkaline
                     phosphatase (BAP) and then decapped with tabacco acid
                     pyrophosphatase (TAP). The decapped intact mRNA was
                     ligated with DNA-RNA linker including EcoR I site by
                     treatment of T4 RNA ligase and the first strand cDNA was
                     synthesized from oligo dT-selected mRNA by priming with
                     dT-tailed vector. The dT-tailed vector was adjusted to
                     have about 60nt. The cDNA vector was circularized with E.
                     coli DNA ligase after digestion of EcoRI which site is
                     also included in vector. An RNA strand converted to a DNA
                     strand by Okayama-Berg method. The obtained cDNA vectors
                     were used for transformation of competent cells E. coli
                     Top10F' by electroporation method. The cDNA libraries
                     constructed by this method are full-length enriched cDNA
                     library."
ORIGIN

  Query Match             100.0%;  Score 190;  DB 4;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 279

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 339

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 399

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        400 TGTTACGCAA 409


RESULT 5
CN409513
LOCUS       CN409513                 638 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN409513
VERSION     CN409513.1  GI:47396637
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 638   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .638
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from embryoid body outgrowths derived from hES cell lines
                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

  Query Match             100.0%;  Score 190;  DB 7;  Length 638;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 287

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 347

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 407

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        408 TGTTACGCAA 417


RESULT 6
BF792159
LOCUS       BF792159                 738 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  602252620F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4344989 5',
            mRNA sequence.
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ACCESSION   BF792159
VERSION     BF792159.1  GI:12097213
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 738)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9964  row: g  column: 06
            High quality sequence stop: 736.
FEATURES             Location/Qualifiers
     source          1. .738
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4344989"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_84"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 190;  DB 2;  Length 738;
  Best Local Similarity   100.0%;  Pred. No. 2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 464

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 524

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 584

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        585 TGTTACGCAA 594


RESULT 7
CN409512
LOCUS       CN409512                751 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000582991415 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN409512
VERSION     CN409512.1  GI:47396636
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 751)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 751   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .751
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, DMSO-treated H9 cell
                     line"
                     /clone_lib="GRN_PREHEP"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from DMSO-treated hES cell line H9 (p22) maintained in
                     feeder-free conditions"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 7;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 589

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 649

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 709

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        710 TGTTACGCAA 719


RESULT 8
AY405891
LOCUS       AY405891                813 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens MTAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY405891
VERSION     AY405891.1  GI:39761865
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 813)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
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  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .813
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>813
                     /gene="MTAP"
                     /locus_tag="HCM2375"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 9;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 510

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 570

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 630

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        631 TGTTACGCAA 640


RESULT 9
BM903599
LOCUS       BM903599               1037 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6622141 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722000
            5', mRNA sequence.
ACCESSION   BM903599
VERSION     BM903599.1  GI:19352956
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12707  row: f  column: 17
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
     source          1. .1037
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5722000"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
ORIGIN

  Query Match             100.0%;  Score 190;  DB 4;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 596

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 656

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 716

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        717 TGTTACGCAA 726


RESULT 10
BM925551
LOCUS       BM925551               1047 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6710137 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5763749
            5', mRNA sequence.
ACCESSION   BM925551
VERSION     BM925551.1  GI:19375930
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12816  row: b  column: 06
            High quality sequence stop: 705.
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5763749"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
```

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ORIGIN

  Query Match            100.0%;  Score 190;  DB 4;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 609

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 669

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 729

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        730 TGTTACGCAA 739


RESULT 11
BX459089
LOCUS       BX459089                1064 bp    mRNA    linear   EST 06-MAY-2004
DEFINITION  BX459089 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YH01
            5-PRIME, mRNA sequence.
ACCESSION   BX459089
VERSION     BX459089.2  GI:47066799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1064)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 22, 2003 this sequence version replaced gi:31029072.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE012CD01QP1&c=5445.f.
FEATURES             Location/Qualifiers
     source          1. .1064
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE012YH01"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match            100.0%;  Score 190;  DB 5;  Length 1064;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 479

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 539

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 599

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        600 TGTTACGCAA 609


RESULT 12
AL543068
LOCUS       AL543068                1075 bp    mRNA    linear   EST 24-MAR-2004
DEFINITION  AL543068 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YH04 5-PRIME, mRNA sequence.
ACCESSION   AL543068
VERSION     AL543068.3  GI:45718631
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1075)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31264915.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5445.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DI002DD02QP1&c=5445.f.
FEATURES             Location/Qualifiers
     source          1. .1075
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI002YH04"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match            100.0%;  Score 190;  DB 1;  Length 1075;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 608

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 668

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 728
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Qy        181 TGTTACGCAA 190
              ||||||||||
Db        729 TGTTACGCAA 738


RESULT 13
BC012316
LOCUS       BC012316               1380 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone
            IMAGE:3546198), containing frame-shift errors.
ACCESSION   BC012316
VERSION     BC012316.1  GI:15147365
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1380)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1380)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 8 Row: b Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006025
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3546198"
                     /tissue_type="Placenta, choriocarcinoma"
                     /clone_lib="NIH_MGC_21"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
ORIGIN

  Query Match             100.0%;  Score 190;  DB 3;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-50;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 597

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 657

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 717

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        718 TGTTACGCAA 727


RESULT 14
BM459757
LOCUS       BM459757               910 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6417999 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534393
            5', mRNA sequence.
ACCESSION   BM459757
VERSION     BM459757.1  GI:18508797
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12220  row: m  column: 18
            High quality sequence stop: 679.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5534393"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_71"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
ORIGIN
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Query Match 99.5%; Score 189; DB 4; Length 910;
Best Local Similarity 99.5%; Pred. No. 4.5e-50;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db        531 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 590

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        591 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGNGGG 650

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 710

Qy        181 TGTTACGCAA 190
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Db        711 TGTTACGCAA 720
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RESULT 15
BG501032
LOCUS BG501032 728 bp mRNA linear EST 27-MAR-2001
DEFINITION 602546438F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668825 5', mRNA sequence.
ACCESSION BG501032
VERSION BG501032.1 GI:13462549
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1479 row: 1 column: 10
High quality sequence stop: 722.
FEATURES Location/Qualifiers
source 1. .728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4668825"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 99.2%; Score 188.4; DB 4; Length 728;
Best Local Similarity 99.5%; Pred. No. 6.7e-50;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 60
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Db        249 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAGGGGACAATGGTC 308

Qy         61 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120
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Db        309 ACAATCGAGGGACCTCGTTTTAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 368

Qy        121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGGTTCTTGCTAAGGAGGCTGGAATA 428

Qy        181 TGTTACGCAA 190
              ||||||||||
Db        429 TGTTACGCAA 438
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